

STIC-Biotech/ChemLib

180630

From: Salmon, Katherine D.  
Sent: Monday, February 27, 2006 9:03 AM  
To: STIC-Biotech/ChemLib  
Subject: SEquence Request

Hi, this is a sequence search request for case 10/720424.

1. Please Search Seq ID No. 1
2. please search seq id NO. 8
3. Please search SEQ ID NO. 1 with word hits under 100
4. Please search SEQ ID No. 8 with word hits under 100

Thanks  
Katherine Salmon  
ART UNIT 1634  
Mailbox REM2C70

RECEIVED  
FEB 27 2006  
STIC

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

**This Page Blank (uspi)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:12:24 ; Search time 1167.5 Seconds  
(without alignments)  
1411.957 Million cell updates/sec

Title: US-10-720-424B-1

Perfect score: 29

Sequence: 1 gatggtgatagtagatagacaggttgg 29

Scoring table: OLIGO NUC

Gapop-60.0, Capext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2524774

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

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- 2: gb\_in.\*
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- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_sts.\*
- 11: gb\_sv.\*
- 12: gb\_un.\*
- 13: gb\_vl.\*
- 14: gb\_hlg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	48.3	38	6	I17042 Sequence 53
2	14	48.3	38	6	BD017550 Short-chain
3	14	48.3	87	11	AY041145 Synthetic
4	13	44.8	17	6	AX578544 Sequence
5	13	44.8	17	6	AX579956 Sequence
6	13	44.8	17	6	AX580273 Sequence
7	13	44.8	21	6	A71350 Sequence 1
8	13	44.8	21	6	CQ821559 Sequence
9	13	44.8	41	6	BD181525 Sequences
10	13	44.8	41	6	AR575320 Sequence
11	13	44.8	41	6	AX474340 Sequence
12	13	44.8	42	6	CQ809558 Sequence
13	13	44.8	74	15	NEUMTRMF
14	12	41.4	17	6	AX578545 Sequence
15	12	41.4	17	6	AX579734 Sequence
16	12	41.4	18	6	CQ808544 Sequence
17	12	41.4	18	6	CS125179 Sequence
18	12	41.4	18	6	AX378402 Sequence

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25	12	41.4	31	6	AX665947	AX665947 Sequence
26	12	41.4	34	6	E04767	E04767 Synthetic D
27	12	41.4	41	6	AX514339	AX514339 Sequence
28	12	41.4	41	6	AX519906	AX519906 Sequence
29	12	41.4	48	6	AX230265	AX230265 Sequence
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31	12	41.4	50	6	AX161516	AX161516 Sequence
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33	12	41.4	51	6	AX158711	AX158711 Sequence
34	12	41.4	51	6	AX158712	AX158712 Sequence
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37	12	41.4	51	6	AX161509	AX161509 Sequence
38	12	41.4	51	6	AX161511	AX161511 Sequence
39	12	41.4	51	6	AX161513	AX161513 Sequence
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42	12	41.4	60	6	CQ541463	CQ541463 Sequence
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44	12	41.4	60	6	CQ551666	CQ551666 Sequence
45	12	41.4	65	6	CQ557874	CQ557874 Sequence

#### ALIGNMENTS

#### RESULT 1

I17042 38 bp DNA linear PAT 03-APR-1996  
LOCUS I17042 Sequence 53 from patent US 5484699.  
DEFINITION I17042  
ACCESSION I17042  
VERSION I17042.1 GI:1251950  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 38)  
AUTHORS Bouma,S.R., Joseph,J.L., Marshall,R.L. and Laffler,T.G.  
TITLE Nucleotide sequences useful as type specific probes, PCR primers and LCR probes for the amplification and detection of human papilloma virus, and related kits and methods  
JOURNAL Patent: US 5484699-A 53 16-JAN-1996;  
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Db 1 GATGGTGATATGGT 14  
RESULT 2  
BD017550 38 bp DNA linear PAT 27-AUG-2002  
LOCUS BD017550 Short-chain nucleotide sequence of human papilloma virus.  
DEFINITION BD017550  
ACCESSION BD017550  
VERSION BD017550.1 GI:22558726  
KEYWORDS JP 2001231587-A/53.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified

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REFERENCE
1 (bases 1 to 38)
AUTHORS Joseph,J.L., Borma,S.R., Marshall,R.L. and Rahler,T.G.
TITLE Short-chain nucleotide sequence of human papilloma virus
JOURNAL Patent: JP 2001231587-A 53 28-AUG-2001;
COMMENT ABBOTT LABORATORIES
OS Unidentified
PN JP 2001231587-A/53
PD 28-AUG-2001
PF 31-JAN-2001 JP 2001023849
PR 28-SEP-1990 US 589948,28-SEP-1990 US 590105 PR
28-SEP-1990 US 590253
PI JEFFREY L JOSEPH,STANLEY R BORMA,RONALD L MARSHALL,THOMAS G
PI RAHLER
PC C12N15/09,C12M1/00,C12Q1/68//(C12N15/09,C12R1/93),C12N15/00,
PC (C12N15/00,C12R1/93)
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CC Topology: Linear;
CC Short-chain nucleotide sequence of human papilloma virus FH
Key source Location/Qualifiers
FT 1..38
FT Location/Qualifiers
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DB 1 GATGGTGATGATGCT 14

RESULT 3
AY044145/c
LOCUS AY044145 87 bp DNA linear SYN 15-SEP-2001
DEFINITION Synthetic construct nitrogen regulatory cis element sequence.
ACCESSION AY044145
VERSION AY044145.1 GI:15625236
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE
1 (bases 1 to 87)
AUTHORS Peng,R., Yao,Q., Xiong,A., Li,X. and Fan,H.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-2001) Shanghai Yong Ye Agro-Bioengineering Co.,
Ltd, Shanghai Academy of Agricultural Sciences, Beidi Road 2901,
Shanghai 201106, China
FEATURES
source
1..87
/organism="synthetic construct"
/mol_type="genomic DNA"
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/notes="contains five copies of the nitrogen regulatory
element (TACTA); can be inserted into lacZ reporter
plasmid for yeast one-hybrid system"

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QY 7 GATATGGTAGATAC 20
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DB 43 GATATGGTAGATAC 30

RESULT 4

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AX578544
LOCUS AX578544 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 382 from Patent WO0211674.
ACCESSION AX578544
VERSION AX578544.1 GI:27647746
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1
AUTHORS Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 382 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
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Location/Qualifiers
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QY 10 ATGGTAGATACAG 22
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DB 4 ATGGTAGATACAG 16

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AX579956
LOCUS AX579956 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 1794 from Patent WO0211674.
ACCESSION AX579956
VERSION AX579956.1 GI:27649158
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1
AUTHORS Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 1794 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGGTAGATACAG 22
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DB 2 ATGGTAGATACAG 14

RESULT 6
AX580273

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LOCUS AX580273 17 bp RNA linear PAT 10-JAN-2003  
DEFINITION Sequence 2111 from Patent WO211674.  
ACCESSION AX580273  
VERSION AX580273.1 GI:27649475  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Thompson, J., McSwiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.  
and Grupe, A.  
TITLE Method and reagent for the inhibition of calcium activated chloride  
channel-1 (clca-1)  
JOURNAL Patent: WO 0211674-A 2111 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);  
Thompson, James (US)  
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Qy 10 ATGGTAGATACAG 22  
Db 3 ATGGTAGATACAG 15  
RESULT 7  
A71350  
LOCUS A71350 21 bp DNA linear PAT 07-MAY-1999  
DEFINITION Sequence 1 from Patent WO9811253.  
ACCESSION A71350  
VERSION A71350.1 GI:4774983  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Ernest, I., Remacle, J., Alexandre, I. and Zammattéo, N.  
TITLE METHOD AND KIT FOR DIAGNOSING AND/OR QUANTIFYING BY SANDWICH  
HYBRIDISATION OF NUCLEIC ACID SEQUENCES ON SOLID SUPPORT  
JOURNAL Patent: WO 9811253-A 1 19-MAR-1998;  
ERNEST ISABELLE (BE)  
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Db 9 GATGGTGATATGG 21  
RESULT 8  
CQ821559  
LOCUS CQ821559 21 bp DNA linear PAT 21-JUN-2004  
DEFINITION Sequence 67 from Patent WO2004047863.  
ACCESSION CQ821559  
VERSION CQ821559.1 GI:49019333  
KEYWORDS

SOURCE  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Sahin, U., Tuercel, O. and Koslowski, M.  
TITLE Genetic products differentially expressed in tumors and the use  
thereof  
JOURNAL Patent: WO 2004047863-A 67 10-JUN-2004;  
Ganymed Pharmaceuticals AG (DE)  
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Best Local Similarity 100.0%; Pred. No. 7.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 10 ATGGTAGATACAG 22  
Db 7 ATGGTAGATACAG 19  
RESULT 9  
BD181525  
LOCUS BD181525 41 bp DNA linear PAT 15-MAY-2003  
DEFINITION Sequences and methods for detection of HIV-1.  
ACCESSION BD181525  
VERSION BD181525.1 GI:30792443  
KEYWORDS JP 2002330790-A/1.  
SOURCE Human immunodeficiency virus 1 (HIV-1)  
ORGANISM Human immunodeficiency virus 1  
Viruses; Retro-transcribing viruses; Retroviridae;  
Orthoretrovirinae; Lentivirus; Primate lentivirus group.  
REFERENCE 1 (bases 1 to 41)  
AUTHORS Hellyer, T.J., You, Q. and Harris, J.M.  
TITLE Sequences and methods for detection of HIV-1  
JOURNAL Patent: JP 2002330790-A 1 19-NOV-2002;  
BECTON DICKINSON AND CO  
COMMENT OS Human immunodeficiency virus type 1  
PN JP 2002330790-A/1  
PD 19-NOV-2002  
PF 03-JAN-2002 JP 2002002066  
PR 03-JAN-2001 US 09/757207  
PI TOBIN J HELLYER, QIMIN YOU, JAMES M HARRIS  
PC C12N15/09, C12Q1/68, C12N15/00  
CC Sequences and methods for detection of HIV-1  
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LOCUS       AR575320               41 bp    DNA             linear       PAT 14-DEC-2004
DEFINITION   Sequence 1 from patent US 6770752.
ACCESSION   AR575320
VERSION     AR575320.1  GI:56576305
KEYWORDS     Unknown.
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 41)
AUTHORS     Hellyer,T.J., You,Q. and Harris,J.M.
TITLE       Sequences for detection of HIV-1
JOURNAL     Patent: US 6770752-A 1 03-AUG-2004;
            Becton, Dickinson and Company; Franklin Lakes, NJ
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QY      12  GGTAGATACAGGA 24
Db      23  GGTAGATACAGGA 35

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AX474340
LOCUS       AX474340               41 bp    DNA             linear       PAT 12-AUG-2002
DEFINITION   Sequence 1 from Patent EPL223227.
ACCESSION   AX474340
VERSION     AX474340.1  GI:22213946
KEYWORDS     Human immunodeficiency virus 1 (HIV-1)
SOURCE      Human immunodeficiency virus 1
ORGANISM     Viruses; Retro-transcribing viruses; Retroviridae;
            Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE    1
AUTHORS     Hellyer,T.J., You,Q. and Harris,J.M.
TITLE       Sequences and methods for detection of hiv-1
JOURNAL     Patent: EP 1223227-A 1 17-JUL-2002;
            Becton, Dickinson and Company (US)
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Best Local Similarity 100.0%; Pred. No. 7.1e+03;
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Db      23  GGTAGATACAGGA 35

RESULT 12
CQ809558
LOCUS       CQ809558               42 bp    DNA             linear       PAT 10-MAY-2004
DEFINITION   Sequence 861 from Patent WO2003097790.
ACCESSION   CQ809558
VERSION     CQ809558.1  GI:47114973
KEYWORDS     Nicotiana tabacum (common tobacco)
SOURCE      Nicotiana tabacum
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE    1

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AUTHORS       Inz,D.G., Goossens,A., Oksman-Caldentey,K.M., Haekkinen,S.T. and
              Laakso,I.J.
TITLE         Genes and uses thereof to modulate secondary metabolite
              biosynthesis
JOURNAL       Patent: WO 2003097790-A 861 27-NOV-2003;
              Vlaams Interuniversitair Instituut voor Biotechnologie vz w. (BE);
              VTT Biotechnology (FI)
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QY      4  GGTGATATGGTAG 16
Db      22  GGTGATATGGTAG 34

RESULT 13
NEUMTTRMF/C
LOCUS       NEUMTTRMF              74 bp    tRNA             linear       PLN 20-MAY-1994
DEFINITION   N.crassa mitochondrial initiator Met-tRNA-f.
ACCESSION   K00315
VERSION     K00315.1  GI:175545
KEYWORDS     transfer RNA; transfer RNA-Met.
SOURCE      mitochondrion Neurospora crassa
ORGANISM     Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE    1 (bases 1 to 74)
AUTHORS     Heckman,J.E., Hecker,L.I., Schwartzbach,S.D., Barnett,W.E.,
            Baumstark,B. and Rajshandray,U.L.
TITLE       Structure and function of initiator methionine tRNA from the
            mitochondria of Neurospora crassa
JOURNAL     Cell 13 (1), 83-95 (1978)
PUBMED      145896
COMMENT     Original source text: Neurospora crassa (strain or23-1a)
            mitochondrial tRNA.
            Contributed on tape April 1983 by M.Sprinzl & D.H.Gauss; from their
            entry 1360 in Nucleic Acids Res. 11, r1-r54 (1983). N.crassa mt
            Met-tRNA-f resembles that of eukaryotic organisms in its structure,
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Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16  GATACAGGATTG 28

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Db 66 GATACAGATTG 54  
 17 bp RNA linear PAT 10-JAN-2003  
 Search completed: March 6, 2006, 00:38:39  
 Job time : 1169.5 secs

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 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
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 Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E.  
 and Grupe, A.  
 Method and reagent for the inhibition of calcium activated chloride  
 channel-1 (clca-1)  
 Patent: WO 0211674-A 383 14-FEB-2002;  
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
 Thompson, James (US)  
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 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 TGGTAGATACAG 22  
 11  
 Db 1 TGGTAGATACAG 12

RESULT 15  
 AX579734  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1  
 Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E.  
 and Grupe, A.  
 Method and reagent for the inhibition of calcium activated chloride  
 channel-1 (clca-1)  
 Patent: WO 0211674-A 1572 14-FEB-2002;  
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
 Thompson, James (US)  
 FEATURES  
 source  
 1. .17  
 /organism="Homo sapiens"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:9606"

Query Match 41.4%; Score 12; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 ATGGTAGATACA 21  
 10

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GenCore version 5.1.7.  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:08:34 ; Search time 271.5 Seconds  
(without alignments)  
711.882 Million cell updates/sec

Title: US-10-720-424B-8

Perfect score: 29  
Sequence: 1 ggcgtcagaggtaccatagagccactagg 29

Scoring-table: OLIGO NUC

Gapop 60.0 , Capext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size: 11

Total number of hits satisfying chosen parameters: 5288170

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	29	12	ADQ27978 Human pap
2	17	58.6	24	12	ADQ27979 Human pap
3	14	48.3	33	12	ADQ27982 Human pap
4	13	44.8	65	6	ABN29627 Rat splc
5	13	44.8	93	4	AAK39536 Human bon
6	13	44.8	93	4	AAK13792 Human bra
7	13	44.8	93	6	ABSL3626 Human gen
8	12	41.4	19	3	AAA86383 PCBA HH r
9	12	41.4	19	3	AAA86382 PCBA HH r
10	12	41.4	19	3	AAA86384 PCBA HH r
11	12	41.4	19	5	AAH61545 PCNA HH r
12	12	41.4	19	5	AAH61544 PCNA HH r
13	12	41.4	19	5	AAH61546 PCNA HH r
14	12	41.4	21	14	ACL53645 TRPM4 sir
15	12	41.4	21	14	ACL53388 TRPM4 sir
16	12	41.4	21	14	ACL53646 TRPM4 sir
17	12	41.4	21	14	ACL53644 TRPM4 tar
18	12	41.4	21	14	ACL53386 TRPM4 tar
19	12	41.4	21	14	ACL53387 TRPM4 sir

20	12	41.4	23	13	ADR45742	Strand #3
21	12	41.4	23	14	ADM08970	siRNA-dup
c 22	12	41.4	50	14	ADY22209	Murine fu
c 23	12	41.4	50	14	ADY22200	Murine fu
c 24	12	41.4	60	6	ABN36247	Human spl
c 25	12	41.4	65	6	ABN52768	Mouse spl
c 26	12	41.4	65	6	ABN54463	Mouse spl
c 27	12	41.4	65	6	ABN29150	Rat splc
c 28	12	41.4	68	13	ADR91004	DNA enzym
c 29	11	37.9	11	6	ABV68952	Human ski
c 30	11	37.9	11	12	ADQ34847	Human fac
c 31	11	37.9	15	6	ABL45752	Human MMP
c 32	11	37.9	17	4	AAF99546	Immunosti
c 33	11	37.9	17	6	ABS78262	Angiogene
c 34	11	37.9	17	6	ABL39094	Immunosti
c 35	11	37.9	17	8	ABT37250	Tumour su
c 36	11	37.9	17	9	ACH03084	Immunosti
c 37	11	37.9	17	9	ADB37048	Immunosti
c 38	11	37.9	17	10	ADB41706	Tumour su
c 39	11	37.9	17	10	ADB39774	Tumour su
c 40	11	37.9	17	10	ADB43518	Tumour su
c 41	11	37.9	17	10	ACC52664	Human tum
c 42	11	37.9	17	13	ADU90062	Allergic
c 43	11	37.9	18	2	AAQ37432	Probe Bl-
c 44	11	37.9	18	4	AAH44097	Oryza sat
c 45	11	37.9	18	11	ADM06615	Human PCR

ALIGNMENTS

RESULT 1  
ADQ27978  
ID ADQ27978 standard; DNA; 29 BP.  
XX  
AC ADQ27978;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human papillomavirus genotype detection PCR primer #8.  
XX  
KW ss; primer; detection; diagnosis; amplification;  
KW Human Papillomavirus genotype; cervical-neoplasia;  
KW oncogenic high-risk group.  
XX  
OS Human papillomavirus.  
XX  
PN WO2004050917-Al.  
XX  
PD 17-JUN-2004.  
XX  
PF 28-NOV-2003; 2003WO-KR002608.  
XX  
PR 29-NOV-2002; 2002KR-00075370.  
XX  
31-JUL-2003; 2003KR-00053147.  
(ALBI-) ALBIOMED CO LTD.  
XX  
Lee S, Kim Y, Yu K, Kim S, Cha K, Ko J;  
XX  
WPI; 2004-450746/42.  
XX  
New general primer or primer pair, useful for amplifying and detecting,  
or for use in a nucleic acid amplification process for amplifying Human  
Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV  
genotypes.  
XX  
Claim 2; SEQ ID NO 8; 71pp; English.  
XX  
The invention relates to a general primer or primer pair for amplifying  
and detecting or for use in a nucleic acid amplification process for  
amplifying Human Papillomavirus (HPV) genotypes. The general primers are  
useful for amplifying cervical-neoplasia related HPV genotypes including

CC oncogenic high-risk groups and low-risk groups. The general primers are  
 CC useful for producing amplifying products to DNA of scores of diverse  
 CC oncogenic HPV types and thus detecting the oncogenic HPV types in a  
 CC sample but also to select cervical carcinoma and its pre-stage lesions at  
 CC early stage by improving sensitivity according to HPV types. This  
 CC sequence corresponds to PCR primer used in the invention.  
 XX  
 SQ Sequence 29 BP; 8 A; 7 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 29; DB 12; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCAGAGTTACCATAGAGCCACTAGG 29  
 |||||  
 DB 1 GCCTCAGAGTTACCATAGAGCCACTAGG 29

## RESULT 2

ADQ27979  
 ID ADQ27979 standard; DNA; 24 BP.

XX AC

ADQ27979;

XX DT 09-SEP-2004 (first entry)

XX DE

Human papillomavirus genotype detection PCR primer #9.

XX ss; primer; detection; diagnosis; amplification;

KW Human Papillomavirus genotype; cervical-neoplasia;

KW oncogenic high-risk group.

XX OS

Human papillomavirus.

XX PN

WO2004050917-A1.

XX PD

17-JUN-2004.

XX PF

28-NOV-2003; 2003WO-KR002608.

XX PR

29-NOV-2002; 2002KR-00075370.

XX PR

31-JUL-2003; 2003KR-00053147.

XX PA

(ALBI-) ALBIOMED CO LTD.

XX PI

Lee S, Kim Y, Yu K, Kim S, Cha K, Ko J;

XX WPI; 2004-450746/42.

XX DR

XX The invention relates to a general primer or primer pair for amplifying  
 PT or for use in a nucleic acid amplification process for amplifying Human  
 PT Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV  
 PT genotypes.

XX PS

Claim 2; SEQ ID NO 9; 71pp; English.

XX CC

The invention relates to a general primer or primer pair for amplifying  
 and detecting or for use in a nucleic acid amplification process for  
 CC amplifying Human Papillomavirus (HPV) genotypes. The general primers are  
 CC useful for amplifying cervical-neoplasia related HPV genotypes including  
 CC oncogenic high-risk groups and low-risk groups. The general primers are  
 CC useful for producing amplifying products to DNA of scores of diverse  
 CC oncogenic HPV types and thus detecting the oncogenic HPV types in a  
 CC sample but also to select cervical carcinoma and its pre-stage lesions at  
 CC early stage by improving sensitivity according to HPV types. This  
 CC sequence corresponds to PCR primer used in the invention.

XX SQ

Sequence 24 BP; 10 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 58.6%; Score 17; DB 12; Length 24;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ACCATAGAGCCACTAGG 29  
 |||||  
 DB 8 ACCATAGAGCCACTAGG 24

## RESULT 3

ADQ27982

ID ADQ27982 standard; DNA; 33 BP.

XX AC

ADQ27982;

XX XX

DT 09-SEP-2004 (first entry)

XX DE

Human papillomavirus genotype detection PCR primer #12.

XX ss; primer; detection; diagnosis; amplification;

KW Human Papillomavirus genotype; cervical-neoplasia;

KW oncogenic high-risk group.

XX OS

Human papillomavirus.

XX PN

WO2004050917-A1.

XX PD

17-JUN-2004.

XX PF

28-NOV-2003; 2003WO-KR002608.

XX PR

29-NOV-2002; 2002KR-00075370.

XX PR

31-JUL-2003; 2003KR-00053147.

XX PA

(ALBI-) ALBIOMED CO LTD.

XX PI

Lee S, Kim Y, Yu K, Kim S, Cha K, Ko J;

XX WPI; 2004-450746/42.

XX DR

New general primer or primer pair, useful for amplifying and detecting,  
 or for use in a nucleic acid amplification process for amplifying Human  
 PT Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV  
 PT genotypes.

XX PS

Claim 2; SEQ ID NO 12; 71pp; English.

XX CC

The invention relates to a general primer or primer pair for amplifying  
 and detecting or for use in a nucleic acid amplification process for  
 CC amplifying Human Papillomavirus (HPV) genotypes. The general primers are  
 CC useful for amplifying cervical-neoplasia related HPV genotypes including  
 CC oncogenic high-risk groups and low-risk groups. The general primers are  
 CC useful for producing amplifying products to DNA of scores of diverse  
 CC oncogenic HPV types and thus detecting the oncogenic HPV types in a  
 CC sample but also to select cervical carcinoma and its pre-stage lesions at  
 CC early stage by improving sensitivity according to HPV types. This  
 CC sequence corresponds to PCR primer used in the invention.

XX SQ

Sequence 33 BP; 13 A; 6 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 48.3%; Score 14; DB 12; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ACCATAGAGCCACT 26

|||||

DB 20 ACCATAGAGCCACT 33

## RESULT 4

ADQ29627/c

ID ADQ29627 standard; DNA; 65 BP.

XX AC

ADQ29627;

XX XX

DT 15-JUL-2002 (first entry)

XX XX

DE Rat spliced transcript detection oligonucleotide SEQ ID NO:2375.  
 XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX Rattus norvegicus.  
 OS  
 PN WO200210449-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 XX 20-JUL-2001; 2001WO-IB001903.  
 XX  
 XX 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX  
 XX (COMP-) COMPUGEN INC.  
 PA  
 XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 PI WPI; 2002-257383/30.  
 XX  
 XX New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX  
 XX Example 1; SEQ ID NO 2375; 47pp; English.  
 PS  
 XX The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridising selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 65 BP; 17 A; 11 C; 21 G; 16 T; 0 U; 0 Other;  
 SQ  
 Query Match 44.8%; Score 13; DB 6; Length 65;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 ACCATAGAGCCAC 25  
 DB 34 ACCATAGAGCCAC 22  
 RESULT 5  
 AAK39536/c  
 ID AAK39536 standard; DNA; 93 BP.  
 XX  
 AC AAK39536;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 XX Human bone marrow expressed single exon probe SEQ ID NO: 14093.

XX Human; bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.  
 XX Homo sapiens.  
 OS  
 PN WO200157276-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 XX 30-JAN-2001; 2001WO-US000668.  
 XX  
 XX 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-488900/53.  
 XX  
 XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human bone marrow.  
 PS  
 XX Example 4; SEQ ID NO 14093; 658pp + Sequence Listing; English.  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
 CC the probes of the invention  
 XX  
 XX Sequence 93 BP; 29 A; 27 C; 15 G; 22 T; 0 U; 0 Other;  
 SQ  
 Query Match 44.8%; Score 13; DB 4; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 ATAGAGCCACTAG 28  
 DB 58 ATAGAGCCACTAG 46  
 RESULT 6  
 AAK13792/c  
 ID AAK13792 standard; DNA; 93 BP.  
 XX  
 AC AAK13792;  
 XX  
 DT 05-NOV-2001 (first entry)  
 XX  
 XX Human brain expressed single exon probe SEQ ID NO: 13783.  
 DE  
 XX Human; brain expressed exon; gene expression analysis; probe; microarray;  
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
 KW ss.  
 XX Homo sapiens.  
 OS  
 XX WO200157275-A2.  
 PN  
 XX 09-AUG-2001.  
 PD  
 XX 30-JAN-2001; 2001WO-US000667.  
 PF  
 XX 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR

```

PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
XX Example 4; SEQ ID NO 13783; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
XX Sequence 93 BP; 29 A; 27 C; 15 G; 22 T; 0 U; 0 Other;
SQ
Query Match 44.8%; Score 13; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ATAGAGCCACTAG 28
Db 58 ATAGAGCCACTAG 46
RESULT 7
ABS13626/c
ID ABS13626 standard; DNA; 93 BP.
XX
XX ABS13626;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human genome-derived single exon probe ORF from lung SEQ ID No 13617.
XX
XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease; open reading frame; ORF.
XX
XX Homo sapiens.
OS
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
XX Claim 4; SEQ ID NO 13617; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a single exon probe open reading frame of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 93 BP; 29 A; 27 C; 15 G; 22 T; 0 U; 0 Other;
SQ
Query Match 44.8%; Score 13; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ATAGAGCCACTAG 28
Db 58 ATAGAGCCACTAG 46
RESULT 8
AAA86383
ID AAA86383 standard; DNA; 19 BP.
XX
XX AAA86383;
XX
XX 04-DEC-2000 (first entry)
XX
XX PCBA HH ribozyme binding site #115.
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
XX Mammalia.
OS

```



```
XX WO200032765-A2.
XX
XX
XX PD 08-JUN-2000.
XX
XX PF 06-DEC-1999; 99WO-US028772.
XX
XX PR 04-DEC-1998; 98US-0110954P.
XX
XX PA (IMMU-) IMMUSOL INC.
XX
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
XX DR WPI; 2000-412314/35.
XX
XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX PCNA and Cyclin B1.
XX
XX PS Disclosure; Page 107; 109pp; English.
XX
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
XX CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX CC Representative examples of ribozyme recognition sites are given in
XX CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX CC inhibiting restenosis by introduction of the ribozyme into cells. The
XX CC ribozyme is resistant to endonuclease activity and hence is efficient in
XX CC restenosis treatment
XX
XX SQ Sequence 19 BP; 7 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 41.4%; Score 12; DB 3; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 10 GTTACCATAGAG 21
XX |||||||||
XX Db 7 GTTACCATAGAG 18
XX
XX RESULT 9
XX ID AAA86382 standard; DNA; 19 BP.
XX
XX AC AAA86382;
XX
XX DT 04-DEC-2000 (first entry)
XX
XX DE PCBA HH ribozyme binding site #114.
XX
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
XX OS Mammalia.
XX
XX PN WO200032765-A2.
XX
XX PD 08-JUN-2000.
XX
XX PF 06-DEC-1999; 99WO-US028772.
XX
XX PR 04-DEC-1998; 98US-0110954P.
XX
XX PA (IMMU-) IMMUSOL INC.
XX
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
XX DR WPI; 2000-412314/35.
XX
XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX KW RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX OS PCNA and Cyclin B1.
XX
XX PS Disclosure; Page 107; 109pp; English.
XX
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
XX CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX CC Representative examples of ribozyme recognition sites are given in
XX CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX CC inhibiting restenosis by introduction of the ribozyme into cells. The
XX CC ribozyme is resistant to endonuclease activity and hence is efficient in
XX CC restenosis treatment
XX
XX SQ Sequence 19 BP; 7 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 41.4%; Score 12; DB 3; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 10 GTTACCATAGAG 21
XX |||||||||
XX Db 7 GTTACCATAGAG 18
XX
XX RESULT 9
XX ID AAA86382 standard; DNA; 19 BP.
XX
XX AC AAA86382;
XX
XX DT 04-DEC-2000 (first entry)
XX
XX DE PCBA HH ribozyme binding site #114.
XX
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
XX OS Mammalia.
XX
XX PN WO200032765-A2.
XX
XX PD 08-JUN-2000.
XX
XX PF 06-DEC-1999; 99WO-US028772.
XX
XX PR 04-DEC-1998; 98US-0110954P.
XX
XX PA (IMMU-) IMMUSOL INC.
XX
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
XX DR WPI; 2000-412314/35.
XX
XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX KW RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX OS PCNA and Cyclin B1.
XX
XX PS Disclosure; Page 107; 109pp; English.
XX
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
XX CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX CC Representative examples of ribozyme recognition sites are given in
XX CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX CC inhibiting restenosis by introduction of the ribozyme into cells. The
XX CC ribozyme is resistant to endonuclease activity and hence is efficient in
XX CC restenosis treatment
XX
XX SQ Sequence 19 BP; 7 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 41.4%; Score 12; DB 3; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 10 GTTACCATAGAG 21
XX |||||||||
XX Db 8 GTTACCATAGAG 19
XX
XX RESULT 10
XX ID AAA86384 standard; DNA; 19 BP.
XX
XX AC AAA86384;
XX
XX DT 04-DEC-2000 (first entry)
XX
XX DE PCBA HH ribozyme binding site #116.
XX
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
XX OS Mammalia.
XX
XX PN WO200032765-A2.
XX
XX PD 08-JUN-2000.
XX
XX PF 06-DEC-1999; 99WO-US028772.
XX
XX PR 04-DEC-1998; 98US-0110954P.
XX
XX PA (IMMU-) IMMUSOL INC.
XX
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
XX DR WPI; 2000-412314/35.
XX
XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX KW RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX OS PCNA and Cyclin B1.
XX
XX PS Disclosure; Page 107; 109pp; English.
XX
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
XX CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX CC Representative examples of ribozyme recognition sites are given in
XX CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX CC inhibiting restenosis by introduction of the ribozyme into cells. The
XX CC ribozyme is resistant to endonuclease activity and hence is efficient in
XX CC restenosis treatment
XX
XX SQ Sequence 19 BP; 7 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 41.4%; Score 12; DB 3; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 10 GTTACCATAGAG 21
XX |||||||||
XX Db 8 GTTACCATAGAG 19
```

```
Db          2 GTTACCATAGAG 13
RESULT 11
AAH61545
ID AAH61545 standard; DNA; 19 BP.
XX
AC AAH61545;
XX
DT 10-SEP-2001 (first entry)
XX
DE PCNA HH ribozyme binding site SEQ ID NO:3969.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnery;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytosatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 360; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnery, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 7 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 41.4%; Score 12; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTACCATAGAG 21
Db          7 GTTACCATAGAG 18
RESULT 12
AAH61544
ID AAH61544 standard; DNA; 19 BP.
XX
AC AAH61544;
XX
DT 10-SEP-2001 (first entry)
XX
DE PCNA HH ribozyme binding site SEQ ID NO:3968.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnery;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytosatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 360; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnery, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 6 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 41.4%; Score 12; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 100.0%; Pred. No. 2.9e+03;
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GTTACCATAGAG 21
Db 8 GTTACCATAGAG 19
|||||
RESULT 13
AAH61546
ID AAH61546 standard; DNA; 19 BP.
XX
AC AAH61546;
XX
DT 10-SEP-2001 (first entry)
XX
DE PCNA HH ribozyme binding site SEQ ID NO:3970.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antiproliferative; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
PS WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
Example 1; Page 360; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antiproliferative,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
Sequence 19 BP; 7 A; 2 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 41.4%; Score 12; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GTTACCATAGAG 21
Db 8 GTTACCATAGAG 13
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RESULT 14
ACL53645/c
ID ACL53645 standard; RNA; 21 BP.
XX
AC ACL53645;
XX
DT 24-MAR-2005 (first entry)
XX
DE TRPM4 siRNA sense sequence, SEQ ID 14717.
XX
KW Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
KW short interfering RNA; gene silencing.
XX
OS Synthetic.
XX
PN WO2005001092-A2.
XX
PD 06-JAN-2005.
XX
PF 19-MAY-2004; 2004WO-US015645.
XX
PR 20-MAY-2003; 2003US-0471729P.
XX
PA (AMHP ) WYETH.
XX
PI Be X, Wei L, Slonim DK, Howes SH;
XX
DR WPI; 2005-075568/08.
XX
PT Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
XX
Claim 3; SEQ ID NO 14717; 113pp; English.
XX
CC The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/electronic_pct_sequences
XX
Sequence 21 BP; 2 A; 8 C; 4 G; 0 T; 7 U; 0 Other;
Query Match 41.4%; Score 12; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 AGAGCCACTAGG 29
Db 12 AGAGCCACTAGG 1
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ID ACLS3388 standard; RNA; 21 BP.
XX
AC ACLS3388;
XX
DT 24-MAR-2005 (first entry)
XX
DE TRPM4 siRNA antisense sequence, SEQ ID 14460.
XX.
KW Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
KW short interfering RNA; gene silencing.
XX
OS Synthetic.
XX
PN WO2005001092-A2.
XX
PD 06-JAN-2005.
XX
PF 19-MAY-2004; 2004WO-US015645.
XX
PR 20-MAY-2003; 2003US-0471729P.
XX
PA (AMHP ) WYETH.
XX
PI Be X, Wei L, Slonim DK, Howes SH;
XX
DR WPI; 2005-075568/08.
XX
PT Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABCA4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
XX
PS Claim 3; SEQ ID NO 14460; 113pp; English.
XX
CC The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABCA4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21 BP; 5 A; 6 C; 6 G; 0 T; 4 U; 0 Other;
Query Match 41.4%; Score 12; DB 14; Length 21;
Best Local Similarity 91.7%; Pred. No. 2.9e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 18 AGAGCCACTAGG 29
DB 2 AGAGCCACUAGG 13
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Job time : 273.5 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:21:59 ; Search time 360 Seconds  
(without alignments)  
666.144 Million cell updates/sec

Title: US-10-720-424B-8

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Gapop 60.0 , Gapext 60.0

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Word size: 11

Total number of hits satisfying chosen parameters: 11327990

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	29	US-10-720-424B-8	Sequence 8, Appli
2	17	58.6	24	US-10-720-424B-9	Sequence 9, Appli
3	15	51.7	25	US-10-719-956-390726	Sequence 390726,
4	14	48.3	33	US-10-720-424B-12	Sequence 12, Appl
5	14	48.3	98	US-09-969-373-1120	Sequence 1120, A
6	13	44.8	25	US-10-719-956-48748	Sequence 48748, A
7	13	44.8	25	US-10-719-956-77937	Sequence 77937, A
8	13	44.8	25	US-10-719-956-100361	Sequence 100361,
9	13	44.8	25	US-10-719-956-587629	Sequence 587629,
10	13	44.8	25	US-10-719-956-590305	Sequence 590305,
11	13	44.8	25	US-10-719-900-203048	Sequence 203048,
12	13	44.8	25	US-10-719-900-295168	Sequence 295168,
13	13	44.8	25	US-10-719-900-403733	Sequence 403733,
14	13	44.8	25	US-10-719-900-968422	Sequence 968422,
15	13	44.8	25	US-10-843-527-84223	Sequence 84223, A
16	13	44.8	25	US-10-843-527-153954	Sequence 153954,
17	13	44.8	25	US-11-036-317-11970	Sequence 11970, A
18	13	44.8	25	US-11-036-317-37797	Sequence 37797, A
19	13	44.8	25	US-11-036-317-48131	Sequence 48131, A
20	13	44.8	25	US-11-036-317-112161	Sequence 112161,
21	13	44.8	25	US-11-036-317-760555	Sequence 760555,
22	13	44.8	25	US-11-036-317-868243	Sequence 868243,
23	13	44.8	25	US-11-036-317-870363	Sequence 870363,

ALIGNMENTS

RESULT 1  
US-10-720-424B-8  
; Sequence 8, Application US/10720424B  
; Publication No. US20040248085A1  
; GENERAL INFORMATION:  
; APPLICANT: ALBIONED CO., LTD  
; APPLICANT: Lee, Sang-Wha  
; APPLICANT: Kim, Yeon-Soo  
; APPLICANT: Yu, Kang-Yeol  
; APPLICANT: Kim, Seung-Jo  
; APPLICANT: Cha, Kwang-Yul  
; APPLICANT: Ko, Jung-Jae  
; TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF  
; FILE REFERENCE: NEI70018  
; CURRENT APPLICATION NUMBER: US/10/720, 424B  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: KR10-2002-0075370  
; PRIOR FILING DATE: 2002-11-29  
; PRIOR APPLICATION NUMBER: KR10-2003-0053147  
; PRIOR FILING DATE: 2003-07-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Human Papillomavirus  
US-10-720-424B-8  
Query Match 100.0%; Score 29; DB 8; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCGTCAGAGGTTTACCATAGGCACTAGG 29  
|||||  
Db 1 GCGTCAGAGGTTTACCATAGGCACTAGG 29  
|||||  
RESULT 2  
US-10-720-424B-9  
; Sequence 9, Application US/10720424B  
; Publication No. US20040248085A1  
; GENERAL INFORMATION:  
; APPLICANT: ALBIONED CO., LTD  
; APPLICANT: Lee, Sang-Wha  
; APPLICANT: Kim, Yeon-Soo

```
; APPLICANT: Yu, Kang-Yeol
; APPLICANT: Kim, Seung-Jo
; APPLICANT: Cha, Kwang-Yul
; APPLICANT: Ko, Jung-Jae
; TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR
; FILE REFERENCE: NEIT0018
; CURRENT APPLICATION NUMBER: US/10/720,424B
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: KR10-2002-0075370
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: KR10-2003-0053147
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 9
; TYPE: DNA
; ORGANISM: Human Papillomavirus
US-10-720-424B-9

Query Match 58.6%; Score 17; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ACCATAGGCCACTAGG 29
DB 8 ACCATAGGCCACTAGG 24

RESULT 3
US-10-719-956-390726/c
; Sequence 390726, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 390726
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-390726

Query Match 51.7%; Score 15; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CATAGAGCCACTAGG 29
DB 19 CATAGAGCCACTAGG 5

RESULT 4
US-10-720-424B-12
; Sequence 12, Application US/10720424B
; Publication No. US20040248085A1
; GENERAL INFORMATION:
; APPLICANT: ALBIOMED CO., LTD
; APPLICANT: Lee, Sang-Wha
; APPLICANT: Kim, Yeon-Soo
; APPLICANT: Yu, Kang-Yeol
; APPLICANT: Kim, Seung-Jo
; APPLICANT: Cha, Kwang-Yul
; APPLICANT: Ko, Jung-Jae
; TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR
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; FILE REFERENCE: NEIT0018
; CURRENT APPLICATION NUMBER: US/10/720,424B
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: KR10-2002-0075370
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: KR10-2003-0053147
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 12
; TYPE: DNA
; ORGANISM: Human Papillomavirus
US-10-720-424B-12

Query Match 48.3%; Score 14; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ACCATAGGCCACT 26
DB 20 ACCATAGGCCACT 33

RESULT 5
US-09-969-373-1120
; Sequence 1120, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10152679/A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1120
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1120

Query Match 48.3%; Score 14; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTACCATAGGCCA 24
DB 63 TTACCATAGGCCA 76

RESULT 6
US-10-719-956-48748/c
; Sequence 48748, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48748
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-48748

Query Match
Best Local Similarity 44.8%; Score 13; DB 7; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTCAGAGGTTACC 15
Db 15 GTCAGAGGTTACC 3

RESULT 7
US-10-719-956-77937
; Sequence 77937, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 77937
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-77937

Query Match
Best Local Similarity 44.8%; Score 13; DB 7; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTCAGAGGTTACC 15
Db 9 GTCAGAGGTTACC 21

RESULT 8
US-10-719-956-100361
; Sequence 100361, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 100361
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-100361

Query Match
Best Local Similarity 44.8%; Score 13; DB 7; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCATAGAGCCACT 26
Db 11 CCATAGAGCCACT 23

RESULT 9
US-10-719-956-587629/c
; Sequence 587629, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 587629
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-587629

Query Match
Best Local Similarity 44.8%; Score 13; DB 7; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCAGAGGTTACCA 16
Db 20 TCAGAGGTTACCA 8

RESULT 10
US-10-719-956-590305
; Sequence 590305, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 590305
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-590305

Query Match
Best Local Similarity 44.8%; Score 13; DB 7; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ACCATAGAGCCAC 25
Db 9 ACCATAGAGCCAC 21

RESULT 11
US-10-900-203048/c
; Sequence 203048, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 203048
; LENGTH: 25
; TYPE: DNA
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; ORGANISM: Mus musculus
US-10-719-900-203046

Query Match      44.8%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGGTTACCAT 17
   |||||
Db 22 CAGAGGTTACCAT 10

RESULT 12
US-10-719-900-295168/c
; Sequence 295168, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 295168
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-295168

Query Match      44.8%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCATAGAGCCACT 26
   |||||
Db 17 CCATAGAGCCACT 5

RESULT 13
US-10-719-900-403733
; Sequence 403733, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 403733
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-403733

Query Match      44.8%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CATAGAGCCACTA 27
   |||||
Db 12 CATAGAGCCACTA 24

RESULT 14
US-10-719-900-968422
; Sequence 968422, Application US/10719900
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 968422
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-968422

Query Match      44.8%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CATAGAGCCACTA 27
   |||||
Db 12 CATAGAGCCACTA 24

RESULT 15
US-10-843-527-84223/c
; Sequence 84223, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 84223
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-84223

Query Match      44.8%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTA 13
   |||||
Db 14 GCGTCAGAGGTTA 2

Search completed: March 5, 2006, 23:01:35
Job time : 361 secs
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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:22:58 ; Search time 449.5 Seconds  
(without alignments)  
141.451 Million cell updates/sec

Title: US-10-720-424B-8

Perfect score: 29  
Sequence: 1 ggcgcaggggtaccatagaccactagg 29

Scoring table: OLIGO NUC  
Gapop 60.0, Gapext 60.0

Searched: 7218535 seqs, 1096242582 residues

Word size: 11

Total number of hits satisfying chosen parameters: 11082884

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Published Applications NA New.\*

- 1: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 5: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 7: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 9: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 11: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	44.8	19	10	US-11-101-244-1039686
2	13	44.8	19	11	US-11-083-784-1039686
3	13	44.8	25	12	US-11-121-849-210096
4	13	44.8	25	12	US-11-121-849-235837
5	13	44.8	25	12	US-11-121-849-417792
6	13	44.8	25	12	US-11-136-527-105826
7	13	44.8	25	12	US-11-136-527-105827
8	13	44.8	25	12	US-11-136-527-105834
9	13	44.8	25	12	US-11-136-527-105835
10	13	44.8	25	12	US-11-136-527-307733
11	13	44.8	25	12	US-11-136-527-307741
12	13	44.8	50	12	US-11-175-859-37597
13	13	44.8	63	9	US-11-173-887-37
14	13	44.8	63	9	US-11-173-887-49
15	12	41.4	18	8	US-10-310-914A-1107332
16	12	41.4	19	8	US-10-310-914A-111205
17	12	41.4	19	10	US-11-101-244-79718
18	12	41.4	19	10	US-11-101-244-79729
19	12	41.4	19	10	US-11-101-244-79757
20	12	41.4	19	10	US-11-101-244-79763

c	21	12	41.4	19	10	US-11-101-244-118485	Sequence 118485,
c	22	12	41.4	19	10	US-11-101-244-139751	Sequence 139751,
	23	12	41.4	19	10	US-11-101-244-165432	Sequence 165432,
	24	12	41.4	19	10	US-11-101-244-165442	Sequence 165442,
	25	12	41.4	19	10	US-11-101-244-165526	Sequence 165526,
	26	12	41.4	19	10	US-11-101-244-333291	Sequence 333291,
	27	12	41.4	19	10	US-11-101-244-360130	Sequence 360130,
	28	12	41.4	19	10	US-11-101-244-360145	Sequence 360145,
	29	12	41.4	19	10	US-11-101-244-360149	Sequence 360149,
	30	12	41.4	19	10	US-11-101-244-490989	Sequence 490989,
	31	12	41.4	19	10	US-11-101-244-491087	Sequence 491087,
c	32	12	41.4	19	10	US-11-101-244-581754	Sequence 581754,
	33	12	41.4	19	10	US-11-101-244-1192442	Sequence 1192442,
	34	12	41.4	19	10	US-11-101-244-1192476	Sequence 1192476,
	35	12	41.4	19	10	US-11-101-244-1192502	Sequence 1192502,
c	36	12	41.4	19	10	US-11-101-244-1195364	Sequence 1195364,
	37	12	41.4	19	10	US-11-101-244-1255833	Sequence 1255833,
	38	12	41.4	19	10	US-11-101-244-1306392	Sequence 1306392,
	39	12	41.4	19	10	US-11-101-244-1472078	Sequence 1472078,
	40	12	41.4	19	11	US-11-083-784-79718	Sequence 79718, A
	41	12	41.4	19	11	US-11-083-784-79729	Sequence 79729, A
	42	12	41.4	19	11	US-11-083-784-79757	Sequence 79757, A
	43	12	41.4	19	11	US-11-083-784-79763	Sequence 79763, A
c	44	12	41.4	19	11	US-11-083-784-118485	Sequence 118485,
c	45	12	41.4	19	11	US-11-083-784-139751	Sequence 139751,

ALIGNMENTS

RESULT 1  
US-11-101-244-1039686  
; Sequence 1039686, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scarlance, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1039686  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1039686  
  
Query Match 44.8%; Score 13; DB 10; Length 19;  
Best Local Similarity 76.9%; Pred. No. 1.8e+02;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 AGGTACCATAGA 20  
Db 7 AGGUACCAUGA 19  
|||||  
|  
  
RESULT 2  
US-11-083-784-1039686  
; Sequence 1039686, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/302,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1039686  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1039686

Query Match 44.8%; Score 13; DB 11; Length 19;  
Best Local Similarity 76.9%; Pred. No. 1.8e+02;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 AGGTTACCATAGA 20  
||||:|||||  
Db 7 AGGUACCAUAGA 19

## RESULT 3

US-11-121-849-210096  
; Sequence 210096, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:

; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 210096  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-210096

Query Match 44.8%; Score 13; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AGGTTACCATAGA 20  
||||:|||||  
Db 7 AGGTTACCATAGA 19

## RESULT 4

US-11-121-849-235837/c  
; Sequence 235837, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:

; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949

; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 235837  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-235837

Query Match 44.8%; Score 13; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCATAGAGCCACT 26  
||||:|||||  
Db 14 CCATAGAGCCACT 2

## RESULT 5

US-11-121-849-417792/c  
; Sequence 417792, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:

; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded E  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 417792  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-417792

Query Match 44.8%; Score 13; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGGTTACCAT 17  
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Db 24 CAGAGGTTACCAT 12

## RESULT 6

US-11-136-527-105826  
; Sequence 105826, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 105826  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-105826

Query Match 44.8%; Score 13; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TACCATAGAGCCA 24  
|||||  
Db 1 TACCATAGAGCCA 13

## RESULT 7

US-11-136-527-105827  
; Sequence 105827, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 105827  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-105827

Query Match 44.8%; Score 13; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TACCATAGAGCCA 24  
|||||  
Db 2 TACCATAGAGCCA 14

## RESULT 8

US-11-136-527-105834  
; Sequence 105834, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 105834  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-105834

Query Match 44.8%; Score 13; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TACCATAGAGCCA 24  
|||||  
Db 3 TACCATAGAGCCA 15

## RESULT 9

US-11-136-527-105835

; Sequence 105835, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 105835  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-105835

Query Match 44.8%; Score 13; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TACCATAGAGCCA 24  
|||||  
Db 5 TACCATAGAGCCA 17

## RESULT 10

US-11-136-527-307733  
; Sequence 307733, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 307733  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-307733

Query Match 44.8%; Score 13; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TACCATAGAGCCA 24  
|||||  
Db 11 TACCATAGAGCCA 23

## RESULT 11

US-11-136-527-307741  
; Sequence 307741, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 307741  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-307741

Query Match 44.8%; Score 13; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TACCATAGAGCCA 24  
|||||  
DB 10 TACCATAGAGCCA 22

RESULT 12  
US-11-175-859-37597  
; Sequence 37597, Application US/11175859  
; Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; PRIOR FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 37597  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-37597

Query Match 44.8%; Score 13; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TACCATAGAGCCA 24  
|||||  
DB 31 TACCATAGAGCCA 43

RESULT 13  
US-11-173-887-37  
; Sequence 37, Application US/11173887  
; Publication No. US20060029954A1  
; GENERAL INFORMATION:  
; APPLICANT: LAO, KAI QIN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING NUCLEOTIDES IN  
; FILE REFERENCE: 375461-017US  
; CURRENT APPLICATION NUMBER: US/11/173,887  
; PRIOR FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,643  
; PRIOR FILING DATE: 2004-06-30  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 37  
; LENGTH: 63  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;

US-11-173-887-37

Query Match 44.8%; Score 13; DB 9; Length 63;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCAGAGGTTACCA 16  
|||||  
DB 44 TCAGAGGTTACCA 56

RESULT 14  
US-11-173-887-49  
; Sequence 49, Application US/11173887  
; Publication No. US20060029954A1  
; GENERAL INFORMATION:  
; APPLICANT: LAO, KAI QIN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING NUCLEOTIDES IN  
; FILE REFERENCE: 375461-017US  
; CURRENT APPLICATION NUMBER: US/11/173,887  
; PRIOR FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,643  
; PRIOR FILING DATE: 2004-06-30  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 49  
; LENGTH: 63  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-11-173-887-49

Query Match 44.8%; Score 13; DB 9; Length 63;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCAGAGGTTACCA 16  
|||||  
DB 44 TCAGAGGTTACCA 56

RESULT 15  
US-10-310-914A-1107332/c  
; Sequence 1107332, Application US/10310914A  
; Publication No. US2006003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1107332  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1107332

Query Match 41.4%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGGTTACCA 16  
|||||  
DB 16 CAGAGGTTACCA 5

Search completed: March 5, 2006, 22:48:30  
Job time : 450.5 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	27.4	94.5	673	13	DQ003076		DQ003076 Human pap
2	27.4	94.5	1546	13	AF070938		AF070938 Human pap
3	27.4	94.5	3891	13	HPU40822		U040822 Human papil
4	27.4	94.5	7759	13	HPU37488		U37488 Human papil
5	27.4	94.5	7887	13	AF436130		AF436130 Human pap
6	27.4	94.5	7889	13	AF020905		AF020905 Common ch
7	27.4	94.5	7966	13	AF419338		AF419338 Human pap
8	27.4	94.5	7975	13	AJ620205		AJ620205 Human pap
9	25.8	89.0	38	6	117042		117042 Sequence 53
10	25.8	89.0	38	6	D017550		D017550 Short-cha
11	25.8	89.0	386	6	A91822		A91822 Sequence 2
12	25.8	89.0	386	6	AR216808		AR216808 Sequence
13	25.8	89.0	386	6	AR216809		AR216809 Sequence
14	25.8	89.0	386	6	BD023226		BD023226 Papilloma
15	25.8	89.0	386	13	HPV295953		Z95953 Human papil
16	25.8	89.0	587	13	DQ003068		DQ003068 Human pap
17	25.8	89.0	807	13	DQ003075		DQ003075 Human pap
18	25.8	89.0	927	13	DQ003078		DQ003078 Human pap

Db	530	GATGGTATGATGATAGATAGATTGG	558	ORGANISM	Human papillomavirus type 74 Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; Alphapapillomavirus. 1 (bases 1 to 3891) Longuet,M., Cassonnet,P. and Orth,G. A novel genital human papillomavirus (HPV), HPV type 74, found in immunosuppressed patients J. Clin. Microbiol. 34 (7), 1859-1862 (1996) JOURNAL PUBMED 8784613 REFERENCE 2 (bases 1 to 3891) Longuet,M., Cassonnet,P. and Orth,G. Direct Submission TITLE JOURNAL Submitted (17-NOV-1995) Michele Longuet, Laboratoire des Papillomavirus, Institut Pasteur, 25 Rue du Dr Roux, Paris 75015, France
RESULT 2	AF070938	1546 bp	DNA	linear	VRL 30-SEP-1998
LOCUS	AF070938				
DEFINITION	Human papillomavirus late major capsid protein (L1) gene, complete cds.				
ACCESSION	AF070938				
VERSION	AF070938.1	GI:3676538			
KEYWORDS					
SOURCE	Human papillomavirus				
ORGANISM	Human papillomavirus				
REFERENCE	1 (bases 1 to 1546)				
AUTHORS	Feoli-Fonseca,J.C., Oligny,L.L., Filion,M., Simard,P., Russo,P.A. and Yotov,W.V.				
TITLE	JC9813-A putative novel human papillomavirus identified by PCR-DS				
JOURNAL	Biochem. Biophys. Res. Commun. 250 (1), 63-67 (1998)				
PUBMED	9735332				
REFERENCE	2 (bases 1 to 1546)				
AUTHORS	Feoli-Fonseca,J.C., Oligny,L.L., Filion,M., Simard,P., Russo,P.A. and Yotov,W.V.				
TITLE	Direct Submission				
JOURNAL	Submitted (05-JUN-1998) Cancer Center Charles Bruneau, Hospital Ste-Justine, 3175 Cote Ste-Catherine, Montreal, QC H3T 1C5, Canada				
FEATURES	Location/Qualifiers				
source	1..1546				
	/organism="Human papillomavirus"				
	/mol_type="genomic DNA"				
	/strain="JC9813"				
	/db_xref="taxon:10566"				
	/notes="identified in 1997 in a cervical biopsy from a 38-year old English Canadian woman, HIV-positive since 1988; pathological diagnosis LSIL"				
gene	8..1516				
	/genes="L1"				
CDS	8..1516				
	/genes="L1"				
	/codon_start=1				
	/product="late major capsid protein"				
	/protein_id="AAC62011.1"				
	/db_xref="GI:3676539"				
	/translation="MMRLNDKVVLPDPGPIASIVSTDYVORTNLFYHAGSSRLAV GHFFPIKNSGKVIYPKVSGHQYRVRVKLPDPNPKFGESETLVTSDFQLVMGCVG VEIGRQPLGVGISGHPYLNKYDDIENPSGYGTS PGQDNRENVMADYKOTQLCIVGCT PMGEVWGKVPKSTSGITQGDGPVLEKSEVIEDGMDVDTGTGALDFASLOAKSDV PLDLCNTKSKYDPDYLMAAEPYNSLPFLRREOMFVRHFNKAGTTGDAVQDLYIA GTGNRAKIAGSIYIYTPSGSLVTSDSQLFNKPLMOKAQNNGICFGNQVFTVVDT TRSTNLTLCASTESVLPTTYDNTKFEYLRHABEFDLQIFOLCIITLNPVMTYIHT MDASLLDNWFGVSPSPSGSLDYTFRLANKAITCQKNVPPKAKEDPYKNYTFWVDL TERFSAQLTQFPFLGRFVMQGLRPPRLKSKGRAPSSSSASPASKRKKTKR"				
ORIGIN					
Query Match	94.5%;	Score 27.4;	DB 13;	Length 1546;	
Best Local Similarity	96.6%;	Pred. No. 0.9;			
Matches	28;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
QY	1	GATGGTATGATGATAGATAGATTGG	29		
Db	590	GATGGTATGATGATAGATAGATTGG	618		
RESULT 3	HPU40822	3891 bp	DNA	linear	VRL 15-AUG-1996
LOCUS	HPU40822				
DEFINITION	Human papillomavirus type 74 E6 protein (E6), E7 protein (E7), and L1 protein (L1) genes, complete cds.				
ACCESSION	U40822				
VERSION	U40822.1	GI:1491796			
KEYWORDS					
SOURCE	Human papillomavirus type 74				
ORGANISM	Human papillomavirus type 74				
REFERENCE	1 (bases 1 to 3891)				
AUTHORS	Longuet,M., Cassonnet,P. and Orth,G. A novel genital human papillomavirus (HPV), HPV type 74, found in immunosuppressed patients J. Clin. Microbiol. 34 (7), 1859-1862 (1996) JOURNAL PUBMED 8784613 REFERENCE 2 (bases 1 to 3891) Longuet,M., Cassonnet,P. and Orth,G. Direct Submission TITLE JOURNAL Submitted (17-NOV-1995) Michele Longuet, Laboratoire des Papillomavirus, Institut Pasteur, 25 Rue du Dr Roux, Paris 75015, France				
FEATURES	Location/Qualifiers				
source	1..3891				
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	/mol_type="genomic DNA"				
	/db_xref="taxon:44028"				
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	/gene="L1"				
CDS	582..2165				
	/gene="L1"				
	/function="putative major capsid protein"				
	/codon_start=1				
	/product="L1 protein"				
	/protein_id="AAC55126.1"				
	/db_xref="GI:1491797"				
	/translation="MWLFYIHHGILLHANAVNPFCLQWRRPSDQVYVPPAPVS KVISTDAYVTRTNIFYHASSSRLLAGNPYPPIROSNKTVVPKVGQYRVRKVLDPD NPGQDNRVNADYKOTQLCMVCGAPLGEHGWKQCSNVNVPKDCPCALLEITSVI PNKFPALDTSIFDPSSQRLVWACTGLEVRGQPLGIGISHPLLNKLKLDVENSASVAA QDGMVDVTGFGAMNFADLPQIKSDVLDICNTCKYDPDYQLMAADPYGRDLFFLRKE QMFARHFNACGTGVEDIPQDLYIKGTRSTLANAIYFNTPSGSLVSSSTQFNKPFW LQRAQHNNICMGWQLFVTVVDTTRSTNMTVCAPTQSQSPATYNSSDYQYMRHVEE FDLQIFOLCSIKLTAEMAYIHTNPTVLEENFGLTPPNGLTLEDTVYVQSOAIT COKPTDRAKPNPYANLFWFVNLKEKFSSELDQYPLGRKFLQITGVQARSSVRVSKK RSAPTAPSSATQKRRKR"				
gene	2948..3400				
	/gene="E6"				
CDS	2948..3400				
	/gene="E6"				
	/function="putative transforming protein"				
	/codon_start=1				
	/product="E6 protein"				
	/protein_id="AAC55127.1"				
	/db_xref="GI:1491798"				
	/translation="MESANASTSAKSIDOLCKDCNIPMHNLOISCVFCRKTLSVPVY SPAYKNLIVYRGNPFPPACAIQLEVGKVNFRHFNAGYALTYEETKKSILDLVI RCYLCHKPCHVEKVRHIVERARFIKGNWGRGCFHCWITCENILP"				
gene	3376..3666				
	/gene="E7"				
CDS	3376..3666				
	/gene="E7"				
	/function="putative transforming protein"				
	/codon_start=1				
	/product="E7 protein"				
	/protein_id="AAC55128.1"				
	/db_xref="GI:1491799"				
	/translation="MHGKYSTLKEIVLELQDPDVGVLHCNEQLDSSSEVEDELATQATQ QUTQAYQIVTCGVCNRSRLVYVQTGPDINNLTLLGLTLNLVCLCAPKT"				
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Query Match	94.5%;	Score 27.4;	DB 13;	Length 3891;	
Best Local Similarity	96.6%;	Pred. No. 0.82;			
Matches	28;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
QY	1	GATGGTATGATGATAGATAGATTGG	29		
Db	1239	GATGGTATGATGATAGATAGATTGG	1267		





LOCUS AF436130 7887 bp DNA linear VRL 02-JAN-2003  
DEFINITION Human papillomavirus type 74 subtype AE10, complete genome.

ACCESSION AF436130

VERSION AF436130.1 GI:27462483

KEYWORDS

SOURCE

ORGANISM

Human papillomavirus type 74

Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

Alphapapillomavirus.

1 (bases 1 to 7887)

Terai, M. and Burk, R.D.

Cervical HPV in Evolution; Genomic sequence of AE10, a subtype of

HPV74

Unpublished

2 (bases 1 to 7887)

Burk, R.D. and Terai, M.

Direct Submission

Submitted (22-OCT-2001) Microbiology & Immunology, Albert Einstein

College of Medicine, 1300 Morris Park Avenue, Bronx, New York, NY

10461, USA

Location/Qualifiers

1. .7887

/organism="Human papillomavirus type 74"

/mol\_type="genomic DNA"

/db\_xref="taxon:44028"

/notes="type: 74; subtype: AE10"

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/protein\_id="AA015455.1"

/db\_xref="GI:27462484"

/translation="MESANASTSAKSIDQLCKDCNIPMNLIQISVCFCKTUSCEVY

SPAYKNLYIVYRGNFPAACAI CLELQKVNQFRFNAYAGYALTVEEETKQILDVLI

RCVLCHEKPCHEKVRHILEKARFINKLGTWKGRCILCHWTCWENILP"

429. .716

/gene="E7"

429. .716

/gene="E7"

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/protein\_id="AA015456.1"

/db\_xref="GI:27462485"

/translation="MGKYPYTLKEIVLQLOPVPGLLCNEQLDSSEEEVDELATQATQ

HQPYQIVTCVCCVCKNSRLVVOCTGPDINNHLTLGLTSLVCPICAPRT"

721. .2643

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721. .2643

/gene="E1"

/codon\_start=1

/product="putative replication protein E1"

/protein\_id="AA015457.1"

/db\_xref="GI:27462486"

/translation="MAENTGTEGTCGSGNFWLVEAIVEHTTGOQISREDEDETVEDNGSD

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DISPLDAIKLSNPKVVRRLPETKEITDSGYGSEVEVQTQVESNEPECGGGGQ

GRTEGEETVQSDTQQQTATTRILELLCKNDVRATLLGKFPDQCYGLSYDLIRQF

KNRTVARMLATLNL PEDHMLI EPEKI QSTVAALYWFRRSLSNASIVQGDTPDWITR

QTVHEGADNQPKLADMYQWADNDLDCSEIAFDY AQRADIDANARAFINFCQAK

YVKDCATMCKHYKNAEMKNMKQWLIHYRSKVVEEAGNKPVIQFLKHQNI BFIPLS

KLMLCHGTQKNCIALIVGPPDTGKSCFCMSLILKFLGGTVIVSYNSSSHFQLPCLNA

KVALLDDATQSCWYIDTYMRNLNDGNPMSIDRKHSLALIKCPPLLITYSNLDITKDE

NKYLFSRVSVFPPFPFDRNGNAVYDLCSNWNKCFPTLSASLDIQNSDEDEDDGD

NSQAFRCVPQTVVTV"

2585. .3730

/gene="E2"

2585. .3730

/gene="E2"

/codon\_start=1

/product="putative regulatory protein E2"

/protein\_id="AA015458.1"

/db\_xref="GI:27462487"

/translation="METIAKHLVDVCOEQLLELYEENNNLEKHI QHWKCVRHESVLLH

KAROMGLHHIGMOWVPPLAVSOTKGEHALEMOMTLETLKSAYGMEPMWLTQDTSRBMW  
LAPPKCFKQCOQVEVKYDCKADNIMEYVMKFIYILDGDEWVKVGQVDYRGLYVV  
QGGYKTYITNFTEAKKYGNLQWECVSGSTVICSPASVSTVQDVSLAGPASYPPTT  
TFAQAAPTIVSTTAAEDHDVADPSKPRGRSTNTNTNTNTNSTVTCITNGDSVDSAN  
NNII LANHNNKGRDNCYCRATPIVOLQDPNCLKCFRYRLHDKHKLFLSASTWHM  
NSTPIPTKHALVTLTYANEQQRQQLDTRVLPPTTISYKLGYSMLQLL"

gene 3060. .3485

/gene="E4"

3060. .3485

/gene="E4"

/codon\_start=1

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ORIGIN

Query Match

Best Local Similarity 94.5%; Score 27.4; DB 13; Length 7887;

Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GATGGTGATGATGATAGATACAGATTGG 29

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DB 6170 GATGGTGATGATGATAGATACAGCTTTGG 6198





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ORIGIN
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Query Match          94.5%; Score 27.4; DB 13; Length 7966;
Best Local Similarity 96.6%; Pred. No. 0.76;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATGGTATGATGGTAGATACAGATTGG 29
Db 6453 GATGGTATGATGGTAGATACAGGTTGG 6481

RESULT 8
AJ620205
LOCUS Human papillomavirus type 43 complete genome. 7975 bp DNA circular VRL 15-APR-2005
DEFINITION Human papillomavirus type 43 complete genome.
ACCESSION AJ620205
VERSION AJ620205.1 GI:40804474
KEYWORDS E1 gene; E2 gene; E4 gene; E6 gene; E7 gene; L1 gene; L2 gene; X gene; Y gene.
SOURCE Human papillomavirus type 43
ORGANISM Human papillomavirus type 43
VIRUSES; deDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE 1
AUTHORS Lorincz,A.T., Quinn,A.P., Goldsborough,M.D., Schmidt,B.J. and Temple,G.F.
TITLE Cloning and partial DNA sequencing of two new human papillomavirus types associated with condylomas and low-grade cervical neoplasia
JOURNAL J. Virol. 63 (6), 2829-2834 (1989)
PUBMED 2542593
REFERENCE 2
AUTHORS Matsukura,T., Delius,H. and Sugase,M.
TITLE Cloning and sequencing of the full-length genome of HPV 43
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 7975)
AUTHORS de Villiers,E.M.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-2004) de Villiers E.M., Div. Characterization of Tumorviruses, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 242, Heidelberg, 69120, GERMANY
FEATURES
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CDS

gene
CDS

gene
CDS
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HMGANKGCGRGSSVAEAVEVEEAGATNSQDICEPSRTRIIELFKDKVTVLLG
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/db_xref="UniProt/TREMBL:Q705H5"
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PPMGYWGQVPCNAGSVTQGDGCPVIELKSEVITQDGMVDVTFGAMDFAQLQASKSDV
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94.5%; Score 27.4; DB 13; Length 7975;
Query Match
Best Local Similarity 96.6%; Pred. No. 0.76;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GATGGTGATGCTAGATACAGGATTGG 29
DB 6339 GATGGTGATGCTAGATACAGGATTGG 6367
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RESULT 9
I17042 38 bp DNA linear PAT 03-APR-1996
LOCUS Sequence 53 from patent US 5484699.
DEFINITION I17042
ACCESSION I17042
VERSION I17042.1 GI:1251950
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Bouma,S.R., Joseph,J.L., Marshall,R.L. and Laffler,T.G.
TITLE Nucleotide sequences useful as type specific probes, PCR primers
and LCR probes for the amplification and detection of human
papilloma virus, and related kits and methods
JOURNAL Patent: US 5484699-A 53 16-JAN-1996;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 89.0%; Score 25.8; DB 6; Length 38;
Best Local Similarity 93.1%; Pred. No. 6.1;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 1 GATGGTGATGCTAGATACAGGATTGG 29
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RESULT 10
BD017550 38 bp DNA linear PAT 27-AUG-2002
LOCUS Short-chain nucleotide sequence of human papilloma virus.
DEFINITION BD017550
ACCESSION BD017550.1 GI:22558726
VERSION JP 200231587-A/53.
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 38)
AUTHORS Joseph,J.L., Borna,S.R., Marshall,R.L. and Rahler,T.G.
TITLE Short-chain nucleotide sequence of human papilloma virus
JOURNAL Patent: JP 200231587-A 53 28-AUG-2001;
COMMENT OS Unidentified
PN JP 200231587-A/53
PD 28-AUG-2001
PF 31-JAN-2001 JP 2001023849
PR 28-SEP-1990 US 589948,28-SEP-1990 US 590105 PR
28-SEP-1990 US 590253
PI JEFFREY L JOSEPH,STANLEY R BORNA,RONALD L MARSHALL,THOMAS G
PI RAHLER
PC C12N15/09,C12M1/00,C12Q1/68//C12N15/09,C12R1:93,C12N15/00,
PC C12N15/00,C12R1:93
CC Strandedness: Single;
CC Topology: Linear;
CC Short-chain nucleotide sequence of human papilloma virus FH
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ORIGIN
source
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Query Match 89.0%; Score 25.8; DB 6; Length 38;  
Best Local Similarity 93.1%; Pred. No. 6.1;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GATGGTGATGATGGTAGATACAGGATTGG 29

RESULT 11  
A91822  
LOCUS A91822 386 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 2 from Patent WO9823752.  
ACCESSION A91822  
VERSION A91822.1 GI:6740700  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 386)  
AUTHORS Zur,H.H. and Lavergne,D.  
TITLE PAPILLOMA VIRUSES, AGENTS FOR DETECTING THE SAME AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES  
JOURNAL Patent: WO 9823752-A 2 04-JUN-1998;  
DEUTSCHES KREBSFORSCH (DE); ZUR HAUSEN HARALD (DE)  
FEATURES  
source Location/Qualifiers  
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ORIGIN  
Query Match 89.0%; Score 25.8; DB 6; Length 386;  
Best Local Similarity 93.1%; Pred. No. 4.8;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 7 GATGGTGATGATGGTAGATACAGGATTGG 35

RESULT 12  
AR216808  
LOCUS AR216808 386 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 4 from patent US 6413522.  
ACCESSION AR216808  
VERSION AR216808.1 GI:23316083  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 386)  
AUTHORS De Villiers-Zur Hausen, E.-M., Zur Hausen, H., Lavergne, D. and Benton, C.  
TITLE Papilloma viruses, products for the detection thereof as well as for treating diseases caused by them  
JOURNAL Patent: US 6413522-A 4 02-JUL-2002;  
Deutsches Krebsforschungszentrum Stiftung des Offentlichen Rechts;  
Heidelberg;  
WOX;  
source Location/Qualifiers  
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## ORIGIN

Query Match 89.0%; Score 25.8; DB 6; Length 386;  
Best Local Similarity 93.1%; Pred. No. 4.8;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 7 GATGGTGATGATGGTAGATACAGGATTGG 35

## RESULT 13

AR216809/c  
LOCUS AR216809 386 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 6 from patent US 6413522.  
ACCESSION AR216809  
VERSION AR216809.1 GI:23316084  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 386)  
AUTHORS De Villiers-Zur Hausen, E.-M., Zur Hausen, H., Lavergne, D. and Benton, C.  
TITLE Papilloma viruses, products for the detection thereof as well as for treating diseases caused by them  
JOURNAL Patent: US 6413522-A 6 02-JUL-2002;  
Deutsches Krebsforschungszentrum Stiftung des Offentlichen Rechts;  
Heidelberg;  
WOX;  
source Location/Qualifiers  
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## ORIGIN

Query Match 89.0%; Score 25.8; DB 6; Length 386;  
Best Local Similarity 93.1%; Pred. No. 4.8;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGGTGATGATGGTAGATACAGGATTGG 29  
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Db 380 GATGGTGATGATGGTAGATACAGGATTGG 352

## RESULT 14

BD023226  
LOCUS BD023226 386 bp DNA linear PAT 27-AUG-2002  
DEFINITION Papilloma virus, reagent for detecting the virus and reagent for treating diseases caused by the virus.  
ACCESSION BD023226  
VERSION BD023226.1 GI:22564449  
KEYWORDS JP 2001505767-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 386)  
AUTHORS Zur,E.M.D.V., Hausen,H.Z., Lavergne,D. and Benton,C.  
TITLE Papilloma virus, reagent for detecting the virus and reagent for treating diseases caused by the virus  
JOURNAL Patent: JP 2001505767-A 2 08-MAY-2001;  
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES EFFENTLICHEN RECHTS  
COMMENT PN JP 2001505767-A/2  
PD 08-MAY-2001  
PF 12-NOV-1997 JP 1998524126  
PR 26-NOV-1996 DE 19648962.8  
PI ETHEL MICHELE DE VILLIERS ZUR HAUSEN, HARALD ZUR HAUSEN, DONNA  
PI LAVERGNE  
PI CLAIRE BENTON  
PC C12N15/09,A61K38/00,A61K39/12,A61K39/395,A61K48/00,  
A61P31/20,

PC C07K14/025,C07K16/08,C12N1/19,C12N1/21,C12N5/10,C12Q1/68, PC

C12N15/00,

PC C12N5/00,A61K37/02

CC Strandedness: Double;

CC Topology: Linear;

CC /desc = 'DNA'

FH Key Location/Qualifiers

FT CDS 1..384.

Location/Qualifiers

1..386

/organism="Homo sapiens"

/mol\_type="genomic DNA"

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Query Match 89.0%; Score 25.8; DB 6; Length 386;

Best Local Similarity 93.1%; Pred. No. 4.8;

Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTGG 29

|||||

Db 7 GATGGTGATATGGTAGACATAGGATTGG 35

RESULT 15

HPV295953

LOCUS 386 bp DNA linear VRL 07-NOV-2004

DEFINITION Human papillomavirus DNA for partial HPV L1 sequence.

ACCESSION 295953

VERSION 295953.1 GI:2664381

KEYWORDS Li.

SOURCE Human papillomavirus

ORGANISM Human papillomavirus

Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

unclassified Papillomaviridae.

REFERENCE 1 (bases 1 to 386)

de Villiers,E.M., Laverne,D., McLaren,K. and Benton,E.C.

Prevailing papillomavirus types in non-melanoma carcinomas of the

skin in renal allograft recipients

Int. J. Cancer 73 (3), 356-361 (1997)

JOURNAL 9359482

PUBMED 9359482

REFERENCE 2 (bases 1 to 386)

de Villiers,E.M.

Direct Submission

Submitted (28-MAY-1997) de Villiers E.M., Deutsches

Krebsforschungszentrum, Tumovirus Charakterisierung 0660, Im

Neuenheimer Feld 242, 69120, Heidelberg, Germany

Location/Qualifiers

1..386

/organism="Human papillomavirus"

/mol\_type="genomic DNA"

/isolate="isolated from Skin squamous cell carcinoma

biopsy, WV-9021; partial HPV L1 seque"

/specific host="Homo sapiens"

/db\_xref="taxon:10566"

/clone\_lib="DL20"

repeat\_region 117..123

ORIGIN

Query Match 89.0%; Score 25.8; DB 13; Length 386;

Best Local Similarity 93.1%; Pred. No. 4.8;

Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTGG 29

|||||

Db 7 GATGGTGATATGGTAGACATAGGATTGG 35



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:50:08 ; Search time 380.5 Seconds  
(without alignments)  
507.953 Million cell updates/sec

Title: US-10-720-424B-1

Perfect score: 29  
Sequence: 1 gatgtgatgtgtacacagattgttg 29

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq\_21.\*

- 1: geneseqn1980s.\*
- 2: geneseqn1990s.\*
- 3: geneseqn2000s.\*
- 4: geneseqn2001as.\*
- 5: geneseqn2001bs.\*
- 6: geneseqn2002as.\*
- 7: geneseqn2002bs.\*
- 8: geneseqn2003as.\*
- 9: geneseqn2003bs.\*
- 10: geneseqn2003cs.\*
- 11: geneseqn2003ds.\*
- 12: geneseqn2004as.\*
- 13: geneseqn2004bs.\*
- 14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	29	12	ADQ27974
2	25.8	89.0	38	2	AAQ23183
3	25.8	89.0	38	2	AAT29878
4	25.8	89.0	386	2	AAV15595
5	25.8	89.0	1421	6	AAI47486
6	25.8	89.0	1497	14	AAI47486
7	25.8	89.0	1524	2	AAT40119
8	25.8	89.0	1950	2	AAQ04472
9	25.8	89.0	2017	1	AAV1804
10	25.8	89.0	7824	14	ADZ45651
11	25.8	89.0	7857	14	ADZ45648
12	25.8	89.0	7880	12	ADN12113
13	25.8	89.0	7896	12	ADN12111
14	24.2	83.4	410	2	AAT47256
15	24.2	83.4	1422	12	ADP89368
16	24.2	83.4	1443	12	ADP89363
17	24.2	83.4	1452	10	ACC47503
18	24.2	83.4	1452	10	ACC47505
19	24.2	83.4	1494	3	AD01237

20	24.2	83.4	1500	3	AD01238
21	24.2	83.4	1506	12	ADP89361
22	24.2	83.4	1515	13	ADP16246
23	24.2	83.4	1515	13	ADP16247
24	24.2	83.4	1517	2	AAQ47167
25	24.2	83.4	1517	2	AAV09856
26	24.2	83.4	1517	2	AAV25817
27	24.2	83.4	1517	2	AAV12161
28	24.2	83.4	1517	2	AAV24099
29	24.2	83.4	1517	2	AAV15112
30	24.2	83.4	1517	3	AAZ40564
31	24.2	83.4	1517	10	ADZ28169
32	24.2	83.4	1517	12	ADG62855
33	24.2	83.4	1518	2	AAZ37566
34	24.2	83.4	1518	3	AAZ48174
35	24.2	83.4	1518	6	ABL58976
36	24.2	83.4	1518	9	ABL11395
37	24.2	83.4	1518	9	ABL11396
38	24.2	83.4	1518	9	ADA27368
39	24.2	83.4	1518	9	ADA92546
40	24.2	83.4	1518	9	ADA14295
41	24.2	83.4	1518	9	ADA58576
42	24.2	83.4	1518	10	ACC47502
43	24.2	83.4	1518	10	ACC47504
44	24.2	83.4	1518	12	ADP83436
45	24.2	83.4	1518	12	ADP83440

ALIGNMENTS

RESULT 1

ADQ27974

ID ADQ27974 standard; DNA; 29 BP.

XX ADQ27974;

XX ADQ27974;

DT 09-SEP-2004 (first entry)

XX Human papillomavirus genotype detection PCR primer #4.

DE ss; primer; detection; diagnosis; amplification;

XX Human Papillomavirus genotype; cervical-neoplasia;

KW oncogenic high-risk group.

KW Human papillomavirus.

XX WO2004050917-Al.

XX 17-JUN-2004.

XX 28-NOV-2003; 2003WO-KR002608.

XX 29-NOV-2002; 2002KR-00075370.

PR 31-JUL-2003; 2003KR-00053147.

XX (ALBI-) ALBIOMED CO LTD.

PI Lee S, Kim Y, Yu K, Kim S, Cha K, Ko J;

XX WPI; 2004-450746/42.

XX New general primer or primer pair, useful for amplifying and detecting,

PT or for use in a nucleic acid amplification process for amplifying Human

PT Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV

XX genotypes.

PS Claim 1; SEQ ID NO 4; 71pp; English.

XX The invention relates to a general primer or primer pair for amplifying

CC and detecting or for use in a nucleic acid amplification process for

CC amplifying Human Papillomavirus (HPV) genotypes. The general primers are

CC useful for amplifying cervical-neoplasia related HPV genotypes including



KW Major capsid protein; detection; infection; disease; wart; cancer; skin;  
 XX diagnosis; treatment; prevention; vaccine; cervix; mouth; throat; ds.  
 XX Human papillomavirus.  
 XX Key Location/Qualifiers  
 XX CDS 1..386  
 FT /\*tag= a  
 FT /product= "major capsid protein"  
 FT /notes= "partial coding sequence"  
 XX DE19648962-C1.  
 XX 26-FEB-1998.  
 XX 26-NOV-1996; 96DE-01048962.  
 XX 26-NOV-1996; 96DE-01048962.  
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX De Villiers- Zur Hausen E, Zur Hausen H, Laverigne D, Benton C;  
 XX WPI: 1998-121621/12.  
 XX P-PSDB; AAW47277.  
 XX DNA encoding peptide(s) from papilloma virus major capsid protein - and  
 PT related proteins, vectors, transformed cells and antibodies, for  
 PT diagnosis, treatment and prevention of papilloma virus infection and  
 PT disease.  
 XX Claim 1; Fig 2; 16pp; German.  
 CC This sequence encodes a fragment of the human papillomavirus (PV) major  
 CC capsid protein isolated from plasmid DL20. This fragment could be used as  
 CC a reagent for detecting PV infections and diseases (e.g. warts or cancers  
 CC of skin, cervix or mouth/throat, particularly of the skin). Cells  
 CC containing transfectants can be used to produce recombinant  
 CC papillomavirus which can be used for diagnosis, treatment and prevention  
 CC (as vaccines) of papillomavirus infection. (Updated on 25-MAR-2003 to  
 CC correct PI field.)  
 XX Sequence 386 BP; 129 A; 62 C; 84 G; 111 T; 0 U; 0 Other;  
 SQ Query Match 89.0%; Score 25.8; DB 2; Length 386;  
 Best Local Similarity 93.1%; Pred. No. 0.34;  
 Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GATGGTATGATGATGATGATGATGATGATGATG 29  
 Db 7 GATGGTATGATGATGATGATGATGATGATGATG 35  
 RESULT 5  
 AAL47486  
 ID AAL47486 standard; DNA; 1421 BP.  
 AC AAL47486;  
 XX 13-SEP-2002 (first entry)  
 DE HPV type 18 L1 gene mutant L1deltaC\*.  
 XX Human papillomavirus type 18; HPV; cancer; L protein; E protein;  
 KW cytostatic; virucide; vaccine; lung; cervix; penis; vulva; anus; gene;  
 KW ds;  
 XX Human papillomavirus type 18.  
 OS Synthetic.  
 XX DE10059630-A1.  
 PN 06-JUN-2002.  
 PT

XX 01-DEC-2000; 2000DE-01059630.  
 XX 01-DEC-2000; 2000DE-01059630.  
 XX (MEDI-) MEDIGENE AG.  
 XX Mueller R, Nieland J, Gabelsberger J, Herbst R;  
 XX WPI: 2002-520969/56.  
 XX P-PSDB; AAO18098.  
 XX Composition for treating and preventing tumors caused by human papilloma  
 PT virus 18, contains fusion protein of papilloma virus L and E proteins,  
 PT preferably truncated.  
 XX Disclosure; Page 14-15; 64pp; German.  
 XX The present invention relates to a composition for preventing or treating  
 CC tumors caused by human papillomavirus (HPV) 18, involving at least one  
 CC fusion protein of at least one each of L and E proteins from one or more  
 CC papillomaviruses, and optionally also additives or auxiliaries. The  
 CC composition can be used as a vaccine to treat or prevent carcinoma of the  
 CC lung, cervix, penis, vulva and anus. The present sequence is an HPV gene  
 XX Sequence 1421 BP; 371 A; 260 C; 316 G; 474 T; 0 U; 0 Other;  
 SQ Query Match 89.0%; Score 25.8; DB 6; Length 1421;  
 Best Local Similarity 93.1%; Pred. No. 0.4;  
 Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GATGGTATGATGATGATGATGATGATGATGATG 29  
 Db 589 GATGGTATGATGATGATGATGATGATGATG 617  
 RESULT 6  
 AEA12674  
 ID AEA12674 standard; DNA; 1497 BP.  
 AC AEA12674;  
 XX 28-JUL-2005 (first entry)  
 DE DNA encoding human papillomavirus 58 L1 protein, 58 L1 wt sequence.  
 XX papillomavirus infection; uterine cervix tumor; carcinoma; HPV58 L1;  
 KW virus-like particle; vaccine; expression; recombinant protein;  
 KW transformation; immune stimulation; virucide; ds; gene.  
 XX Human papillomavirus - 58.  
 XX Key Location/Qualifiers  
 XX CDS 1..1497  
 FT /\*tag= a  
 FT /product= "HPV58 L1"  
 XX WO2005047315-A2.  
 XX 26-MAY-2005.  
 XX 10-NOV-2004; 2004WO-US037372.  
 XX 12-NOV-2003; 2003US-0519211P.  
 XX (MERI) MERCK & CO INC.  
 XX Bryan JT, Brownlow MK, Schultz LD, Wang X, Jansen KU;  
 XX WPI: 2005-372343/38.  
 XX P-PSDB; AEA12673.  
 XX New nucleic acid molecule encoding HPV58 L1, useful for immunoprophylaxis

PT against papillomavirus infection, and for treating existing human  
PT papillomavirus infection.  
XX  
XX  
PS Disclosure; SEQ ID NO 3; 39pp; English.  
XX  
XX The new invention relates to the prevention and therapy of human  
CC papillomavirus (HPV) infection. More than 90% of cervical carcinomas are  
CC associated with infections of HPV31, HPV33, -45, -52, and -58. The L1  
CC protein is the major capsid protein and is highly conserved among  
CC different papillomaviruses. Expression of the L1 and L2 proteins in  
CC yeast, insect, mammal or bacterial cells leads to self-assembly of virus-  
CC like particles (VLPs). VLPs are similar to authentic virions and are  
CC capable of inducing high titres of neutralizing antibodies when  
CC administered into animals, without the potentially oncogenic viral  
CC genome. Therefore, L1 and L2 genes have been identified as immunological  
CC targets for the development of prophylactic and therapeutic vaccines for  
CC HPV infection. Vaccine development has been limited by difficulties in  
CC obtaining high expression levels of capsid proteins. The present  
CC invention provides a nucleic acid (SEQ ID NO:1) encoding HPV58 L1 protein  
CC (SEQ ID NO: 2), which is codon-optimized for high-level expression in  
CC yeast cells. Virus-like particles (VLPs) are also disclosed comprised of  
CC recombinant L1 protein or recombinant L1 + L2 proteins of HPV58.  
CC Described is a method of producing the VLPs by transforming yeast with  
CC the HPV58 L1 gene, and cultivating the yeast under conditions that permit  
CC expression of the protein. Specifically claimed is a vaccine comprising  
CC the VLPs. The gene and vaccine are useful for immunoprophylaxis against  
CC papillomavirus infection, and for treating existing human papillomavirus  
CC infection. The present sequence is DNA encoding human papillomavirus 58  
CC L1 protein, designated 58 L1 wt.  
XX  
XX Sequence 1497 BP; 445 A; 280 C; 310 G; 462 T; 0 U; 0 Other;  
SQ

Query Match 89.0%; Score 25.8; DB 14; Length 1497;  
Best Local Similarity 93.1%; Pred. No. 0.4;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGGTGATATGATGATACACAGATTGG 29  
||||| ||||||| ||||||| |||||  
Db 589 GATGGTGACATGCTAGATACAGGTTGG 617

RESULT 7  
AAAT40119  
ID AAT40119 standard; DNA; 1524 BP.  
XX  
XX AAT40119;  
DT 28-JAN-1997 (first entry)  
XX  
XX Human papillomavirus type 18 L1 capsid protein gene.  
DE  
XX HPV-18; L1 gene; capsid protein; vaccine; diagnosis; vector; antibody;  
XX serotyping; cervix carcinoma; ss.  
KW  
XX Human papillomavirus type 18.  
OS  
XX WO9629413-A2.  
PN  
XX 26-SEP-1996.  
PD  
XX 18-MAR-1996; 96WO-US003649.  
PF  
XX 22-MAR-1995; 95US-00408669.  
PR  
XX 22-MAR-1995; 95US-00409122.  
XX  
XX (MERI ) MERCK & CO INC.  
PA  
XX Hofmann KJ, Jansen KU, Neepser MP, Joyce JG, George HA;  
PI WPI; 1996-443188/44.  
XX P-PSDB; AAW05843.  
DR  
XX DNA encoding human papilloma virus 18, esp. L1 and L2 capsid proteins -

PT and related vectors and antibodies, useful in protective vaccines, for  
PT serotyping HPV infections and as therapeutic agents.  
XX  
XX  
PS Claim 2; Fig 1; 46pp; English.  
XX  
XX The L1 gene (AAT40119) codes for the major capsid protein (AAW05843) of  
CC human papillomavirus type 18 (HPV18), an HPV type associated with  
CC invasive carcinomas of the cervix, vagina, vulva and anal canal. The DNA  
CC sequence was deduced from a genomic clone isolated from human cervical  
CC carcinoma-derived SW756 cells using an HPV18 L1 probe. The HPV18 L1 and  
CC L2 (see also AAT40120) genes can be used in vaccines against HPV18  
CC infection, as probes, or to produce recombinant capsid proteins in host  
CC cells  
XX  
XX Sequence 1524 BP; 396 A; 292 C; 337 G; 499 T; 0 U; 0 Other;  
SQ

Query Match 89.0%; Score 25.8; DB 2; Length 1524;  
Best Local Similarity 93.1%; Pred. No. 0.4;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGGTGATATGATGATACACAGATTGG 29  
||||| ||||||| ||||||| |||||  
Db 589 GATGGTGATGCTAGATACAGGTTGG 617

RESULT 8  
AAQ04472  
ID AAQ04472 standard; DNA; 1950 BP.  
XX  
XX AAQ04472;  
XX  
XX 27-AUG-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 04-OCT-1990 (first entry)  
XX  
XX Human papilloma virus 52 clone pCD15 noncoding region.  
DE  
XX Human papilloma virus type 52; HPV infection; probes; cervical cancer;  
KW ss.  
XX  
XX Human papillomavirus type 52.  
XX  
XX EP370625-A.  
PN  
XX 30-MAY-1990.  
PD  
XX 24-OCT-1989; 89EP-00310934.  
PF  
XX 26-OCT-1988; 88US-00262597.  
PR  
XX (GEOU ) UNIV GEORGETOWN.  
PA  
XX Lancaster WD;  
PI  
XX WPI; 1990-165336/22.  
XX  
XX Human papilloma-virus type 52 DNA and RNA - used in probes for detecting  
PT HPV infection in samples and for blocking HPV gene expression.  
XX  
XX Disclosure; Page ?; -pp; English.  
XX  
XX This partial sequence is from the middle of the L1 ORF through the  
CC noncoding region. Comparison of the sequence of HPV33 and HPV 52 revealed  
CC 75% homology in the L1ORF and less than 50% homology in the noncoding  
CC region. The HPV 52 was isolated and cloned from the combined DNA of  
CC biopsies of 2 mild dysplasias. The DNA was cloned into lambda L47 and  
CC positive plaques by nonstringent hybridisation with HPV-16 probes were  
CC isolated to obtain HPV 52 DNA. The probes obtained from this sequence can  
CC be used for detecting HPV infection in a sample, for assessing the risk  
CC of cancer development, in partic. for detecting HPV 52 which may play a  
CC role in cervical cancer development. The HPV 52 anti-sense RNA or  
CC fragments can be used as blockers or regulators of HPV gene expression in  
CC general and HPV 52 in partic. (Updated on 25-MAR-2003 to correct PA

```
CC field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 1950 BP; 551 A; 376 C; 380 G; 643 T; 0 U; 0 Other;

Query Match      89.0%; Score 25.8; DB 2; Length 1950;
Best Local Similarity 93.1%; Pred. No. 0.42;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGGTGATATGATGATAGATACAGGATTGG 29
Db 138 GATGGGACATGATGATAGATACAGGATTGG 166

RESULT 9
AAN91804
ID AAN91804 standard; DNA; 2017 BP.
XX
AC AAN91804;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-MAR-1990 (first entry)
XX
DE Human papilloma virus type 33 marker fragment.
XX
KW Cervical cancer.
XX
OS Human papillomavirus type 33.
XX
PN W08909940-A.
XX
PD 19-OCT-1989.
XX
PF 04-APR-1989; 89WO-US001318.
XX
PR 04-APR-1988; 88US-00177404.
PR 31-MAR-1989; 89US-00330381.
XX
PA (ONCO-) ONCOR INC.
XX
PI George AL, Groff DE;
XX
DR WPI; 1989-324314/44.
XX
PT Rapid detection of specific human papilloma virus genotypes - by
PT hybridisation of DNA digest with new labelled nucleic acid probes.
XX
PS Disclosure; Fig 23; 81pp; English.
XX
CC Used as a probe. The patent describes probes (DNA or RNA) and their
CC complements capable of detecting one or a combination of HPV types 6, 11,
CC 16, 18, 31, 33 and 35. (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 2017 BP; 583 A; 399 C; 373 G; 662 T; 0 U; 0 Other;

Query Match      89.0%; Score 25.8; DB 1; Length 2017;
Best Local Similarity 93.1%; Pred. No. 0.42;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGGTGATATGATGATAGATACAGGATTGG 29
Db 1453 GATGGTGATATGATGATAGATACAGGATTGG 1481

RESULT 10
AD245651
ID AD245651 standard; DNA; 7824 BP.
XX
AC AD245651;
XX
DT 30-JUN-2005 (first entry)
XX

DE Human papillomavirus type 58 full length genomic clone - SEQ ID 5.
XX
KW tumor marker; genome; diagnosis; cancer; uterine cervix tumor;
KW rectal tumor; colon tumor; ds.
XX
OS Human papillomavirus type 58.
XX
PN W02005033333-A2.
XX
PD 14-APR-2005.
XX
PF 04-OCT-2004; 2004WO-DK000670.
XX
PR 07-OCT-2003; 2003DK-00001474.
PR 13-FEB-2004; 2004US-0543925P.
XX
XX (DAKO-) DAKOCYTOMATION DENMARK AS.
XX
PI Chau MF, Bisgaard-Franzen K, Lin J, Rasmussen OF, Wang Z, Lusk J;
PI Lindberg M, Yeast S;
XX
DR WPI; 2005-285441/29.
XX
XX New composition having a nucleic acid molecule identical to genomic clone
PT of human papilloma virus 16, 18 or 51, useful in diagnosing cancer or the
PT risk of developing cancer, in particular cervical, anal, colon and HPV-
PT related cancer.
XX
PS Claim 2; SEQ ID NO 5; 169pp; English.
XX
XX The invention comprises a composition for the detection of cancer
CC markers, the composition contains a nucleic acid molecule which is
CC substantially identical to a full length genomic clone of a human
CC papilloma virus (type 11, 16, 18, 51, 56, 58, 66, 70, or 73). The
CC composition of the invention is useful for diagnosing cancer or the risk
CC of developing cancer, in particular cervical, anal, colon and HPV-related
CC cancer. The present DNA sequence represents a human papilloma virus full
CC length genomic clone of the invention.
XX
SQ Sequence 7824 BP; 2487 A; 1388 C; 1576 G; 2373 T; 0 U; 0 Other;

Query Match      89.0%; Score 25.8; DB 14; Length 7824;
Best Local Similarity 93.1%; Pred. No. 0.5;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGGTGATATGATGATAGATACAGGATTGG 29
Db 6231 GATGGTGATATGATGATAGATACAGGATTGG 6259

RESULT 11
AD245648
ID AD245648 standard; DNA; 7857 BP.
XX
AC AD245648;
XX
DT 30-JUN-2005 (first entry)
XX
DE Human papillomavirus type 18 full length genomic clone - SEQ ID 2.
XX
KW tumor marker; genome; diagnosis; cancer; uterine cervix tumor;
KW rectal tumor; colon tumor; ds.
XX
OS Human papillomavirus type 18.
XX
PN W02005033333-A2.
XX
PD 14-APR-2005.
XX
PF 04-OCT-2004; 2004WO-DK000670.
XX
PR 07-OCT-2003; 2003DK-00001474.
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PR 07-OCT-2003; 2003US-0509205P.
PR 13-FEB-2004; 2004US-0543925P.
XX
XX (DAKO-) DAKOCYTOMATION DENMARK AS.
XX
XX Chau MF, Bisgaard-Franzen K, Lin J, Rasmussen OF, Wang Z, Lusk J;
PI Lindberg M, Yeast S;
XX WPI; 2005-285441/29.
XX
XX New composition having a nucleic acid molecule identical to genomic clone
PT of human papilloma virus 16, 18 or 51, useful in diagnosing cancer or the
PT risk of developing cancer, in particular cervical, anal, colon and HPV-
PT related cancer.
XX
XX Claim 1; SEQ ID NO 2; 169pp; English.
XX
XX The invention comprises a composition for the detection of cancer
XX markers, the composition contains a nucleic acid molecule which is
XX substantially identical to a full length genomic clone of a human
XX papilloma virus (type 11, 16, 18, 51, 56, 58, 66, 70, or 73). The
XX composition of the invention is useful for diagnosing cancer or the risk
XX of developing cancer, in particular cervical, anal, colon and HPV-related
XX cancer. The present DNA sequence represents a human papilloma virus full
XX length genomic clone of the invention.
XX
XX Sequence 7857 BP; 2365 A; 1497 C; 1680 G; 2315 T; 0 U; 0 Other;
SQ
    Query Match      89.0%; Score 25.8; DB 14; Length 7857;
    Best Local Similarity 93.1%; Pred. No. 0.5;
    Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGGTATGATGGTAGATACAGGATTGG 29
   ||||| ||||| ||||| ||||| |||||
Db 6201 GATGGTATGATGGTAGATACAGGATTGG 6229

RESULT 12
ADN12113
ID ADN12113 standard; DNA; 7880 BP.
XX
XX ADN12113;
XX
XX 17-JUN-2004 (first entry)
XX
XX HPV type 13 genome #1.
XX
XX major histocompatibility class I; MHC-I; MHC-II; Cytostatic;
KW EBV-associated cancer; Hodgkin's lymphoma; nasopharyngeal carcinoma;
KW Gastric carcinoma; Burkitt's lymphoma; T-cell lymphoma; B-cell lymphoma;
KW parotid carcinoma; breast carcinoma; leiomyosarcoma; ds.
XX
XX Human Papilloma Virus.
XX
XX WO2004027036-A2.
XX
XX 01-APR-2004.
XX
XX 19-SEP-2003; 2003WO-US029684.
XX
XX 19-SEP-2002; 2002US-0411990P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Ambinder RF, Yang Y, Borrello IM, Levitsky HI;
XX
XX WPI; 2004-295406/27.
XX
XX New human cell line modified to comprise and express genes encoding
PT immunomodulators and an antigen of Epstein-Barr virus (EBV), useful for
PT inducing or stimulating an immune response in a human to EBV-associated
PT cancer.
XX
XX Example 1; SEQ ID NO 2; 169pp; English.
XX
XX The present invention relates to a human cell line, which lacks major
XX histocompatibility class I(MHC-I) and MHC-II antigens and which has been
XX modified to comprise and express a gene encoding an immunomodulator and a
XX gene encoding an antigen of Epstein-Barr virus (EBV). The human cell
XX line, compositions and methods are useful for inducing or stimulating an
XX immune response in a human to an EBV-associated cancer, where the human
XX has or is at risk for Hodgkin's lymphoma, nasopharyngeal carcinoma,
XX gastric carcinoma, Burkitt's lymphoma, T-cell lymphoma, B-cell lymphoma,
XX parotid carcinoma, breast carcinoma, and leiomyosarcoma. The present
XX sequence represents a nucleotide sequence associated with the cell line
XX of the invention.
XX
XX Sequence 7880 BP; 2452 A; 1480 C; 1628 G; 2320 T; 0 U; 0 Other;
SQ
    Query Match      89.0%; Score 25.8; DB 12; Length 7880;
    Best Local Similarity 93.1%; Pred. No. 0.5;
    Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGGTATGATGGTAGATACAGGATTGG 29
   ||||| ||||| ||||| ||||| |||||
Db 6321 GATGGTATGATGGTAGATACAGGATTGG 6349

RESULT 13
ADN12111
ID ADN12111 standard; DNA; 7896 BP.
XX
XX ADN12111;
XX
XX 17-JUN-2004 (first entry)
XX
XX HPV type 59 genome #1.
XX
XX major histocompatibility class I; MHC-I; MHC-II; Cytostatic;
KW EBV-associated cancer; Hodgkin's lymphoma; nasopharyngeal carcinoma;
KW Gastric carcinoma; Burkitt's lymphoma; T-cell lymphoma; B-cell lymphoma;
KW parotid carcinoma; breast carcinoma; leiomyosarcoma; ds.
XX
XX Human Papilloma Virus.
XX
XX WO2004027036-A2.
XX
XX 01-APR-2004.
XX
XX 19-SEP-2003; 2003WO-US029684.
XX
XX 19-SEP-2002; 2002US-0411990P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Ambinder RF, Yang Y, Borrello IM, Levitsky HI;
XX
XX WPI; 2004-295406/27.
XX
XX New human cell line modified to comprise and express genes encoding
PT immunomodulators and an antigen of Epstein-Barr virus (EBV), useful for
PT inducing or stimulating an immune response in a human to EBV-associated
PT cancer.
XX
XX Example 1; SEQ ID NO 4; 218pp; English.
XX
XX The present invention relates to a human cell line, which lacks major
XX histocompatibility class I(MHC-I) and MHC-II antigens and which has been
XX modified to comprise and express a gene encoding an immunomodulator and a
XX gene encoding an antigen of Epstein-Barr virus (EBV). The human cell
XX line, compositions and methods are useful for inducing or stimulating an
XX immune response in a human to an EBV-associated cancer, where the human
XX has or is at risk for Hodgkin's lymphoma, nasopharyngeal carcinoma,
XX gastric carcinoma, Burkitt's lymphoma, T-cell lymphoma, B-cell lymphoma,
XX parotid carcinoma, breast carcinoma, and leiomyosarcoma. The present
XX sequence represents a nucleotide sequence associated with the cell line
XX of the invention.
XX
XX Sequence 7880 BP; 2452 A; 1480 C; 1628 G; 2320 T; 0 U; 0 Other;
SQ
    Query Match      89.0%; Score 25.8; DB 12; Length 7880;
    Best Local Similarity 93.1%; Pred. No. 0.5;
    Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGGTATGATGGTAGATACAGGATTGG 29
   ||||| ||||| ||||| ||||| |||||
Db 6321 GATGGTATGATGGTAGATACAGGATTGG 6349

```

```

PS Example 1; SEQ ID NO 6; 218pp; English.
XX
XX The present invention relates to a human cell line, which lacks major
XX histocompatibility class I(MHC-I) and MHC-II antigens and which has been
XX modified to comprise and express a gene encoding an immunomodulator and a
XX gene encoding an antigen of Epstein-Barr virus (EBV). The human cell
XX line, compositions and methods are useful for inducing or stimulating an
XX immune response in a human to an EBV-associated cancer, where the human
XX has or is at risk for Hodgkin's lymphoma, nasopharyngeal carcinoma,
XX gastric carcinoma, Burkitt's lymphoma, T-cell lymphoma, B-cell lymphoma,
XX parotid carcinoma, breast carcinoma, and leiomyosarcoma. The present
XX sequence represents a nucleotide sequence associated with the cell line
XX of the invention.
XX
XX Sequence 7880 BP; 2452 A; 1480 C; 1628 G; 2320 T; 0 U; 0 Other;
SQ
    Query Match      89.0%; Score 25.8; DB 12; Length 7880;
    Best Local Similarity 93.1%; Pred. No. 0.5;
    Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGGTATGATGGTAGATACAGGATTGG 29
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Db 6321 GATGGTATGATGGTAGATACAGGATTGG 6349

```

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CC of the invention.
SQ Sequence 7896 BP; 2473 A; 1457 C; 1594 G; 2372 T; 0 U; 0 Other;

Query Match      89.0%; Score 25.8; DB 12; Length 7896;
Best Local Similarity 93.1%; Pred. No. 0.5;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGGTGATATGGTAGATACAGATTGG 29
Db 6194 GATGGTGATATGGTAGATACAGATTGG 6222

RESULT 14
AAT47256
ID AAT47256 standard; DNA; 410 BP.
XX
AC AAT47256;
XX
DT 05-SEP-1997 (first entry)
XX
DE (DSM 10097) human papillomavirus major capsid protein DNA.
XX
KW HPV; major; capsid; L1; HPV48; pVS201-1; DSM 10097; diagnosis; disease;
KW skin cancer; therapy; prevention; vaccination; ss.
XX
OS Human papillomavirus.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..408
FT /tag= a
FT /label= major_capsid_protein
XX
XX DE19526386-C1.
XX
XX 02-JAN-1997.
XX
XX 19-JUL-1995; 95DE-01026386.
XX
XX 19-JUL-1995; 95DE-01026386.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Shamanin V, Villiers-Zur Hausen E, Zur Hausen H;
XX
XX WPI; 1997-043923/05.
XX
XX P-PSDB; AAW07854.
XX
XX DNA encoding peptide(s) of papilloma major capsid protein - useful for
XX diagnosis, treatment and prevention of papilloma virus disease.
XX
XX Claim 1; Fig 3; 15pp; German.
XX
XX The present sequence, which encodes a human papillomavirus (HPV) major
XX capsid (L1) protein, is 69.4% homologous to the HPV48 L1 DNA. The
XX encoding DNA, which is contained in pVS201-1 (DSM 10097), is useful for
XX the diagnosis of HPV diseases, especially skin cancer, and for the
XX preparation of the protein. The protein is useful for the diagnosis,
XX therapy and prevention (by vaccination) of these diseases
XX
XX Sequence 410 BP; 116 A; 69 C; 99 G; 126 T; 0 U; 0 Other;

Query Match      83.4%; Score 24.2; DB 2; Length 410;
Best Local Similarity 89.7%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTGATATGGTAGATACAGATTGG 29
Db 13 GATGGTGATATGGTAGATACAGATTGG 41

RESULT 15
ADF89368
```

```
ID ADF89368 standard; DNA; 1422 BP.
XX
AC ADF89368;
XX
DT 26-FEB-2004 (first entry)
XX
DE Plant-optimised NLS-deleted Human papillomavirus type 16 L1 DNA.
XX
KW papillomavirus virus-like particle; capsomere; transgenic; plant;
KW L1 capsid; gene therapy; HPV16; ds; gene; mutant.
XX
OS Synthetic.
OS Human papillomavirus type 16.
XX
XX Key Location/Qualifiers
XX CDS 1..1422
XX /tag= a
XX /product= "Plant-optimised NLS-deleted Human
XX papillomavirus type 16 L1 protein"
XX
XX WO2003093437-A2.
XX
XX 13-NOV-2003.
XX
XX 02-MAY-2003; 2003WO-US013757.
XX
XX 02-MAY-2002; 2002US-0377467P.
XX
XX (UVRP ) UNIV ROCHESTER.
XX (BOYC-) BOYCE THOMPSON INST PLANT RES INC.
XX
XX Rose RC, Mason HS, Warzecha H;
XX
XX WPI; 2004-011891/01.
XX P-PSDB; ADF89369.
XX
XX Producing papillomavirus virus-like particles or capsomeres comprises
XX providing a transgenic plant or plant seed transformed with a nucleic
XX acid molecule comprising a papillomavirus L1 capsid protein coding
XX sequences.
XX
XX Example 9; SEQ ID NO 8; 74pp; English.
XX
XX The invention relates to a novel method for producing papillomavirus
XX virus-like particles or capsomeres comprising providing a transgenic
XX plant or plant seed transformed with a nucleic acid molecule comprising
XX papillomavirus L1 capsid protein coding sequences and growing the
XX transgenic plant or transgenic plant grown from the transgenic plant seed
XX under conditions effective to produce the virus-like particles containing
XX the papillomavirus L1 capsid protein. The invention may have virucide
XX applications whilst the methods, genetic construct and plant may be
XX useful for immunising a subject against a disease resulting from
XX infection by a papillomavirus, as well as during gene therapy procedures.
XX The current sequence is that of the plant-optimised NLS (nuclear
XX localisation signal)-deleted Human papillomavirus type 16 (HPV16) L1 DNA
XX of the invention.
XX
XX Sequence 1422 BP; 384 A; 343 C; 296 G; 399 T; 0 U; 0 Other;

Query Match      83.4%; Score 24.2; DB 12; Length 1422;
Best Local Similarity 89.7%; Pred. No. 1.9;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTGATATGGTAGATACAGATTGG 29
Db 589 GATGGTGATATGGTAGATACAGATTGG 617

Search completed: March 5, 2006, 22:12:07
Job time : 383.5 secs
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**This Page Blank (uspto)**



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd..

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:59:29 ; Search time 3168 Seconds  
(without alignments)  
428.291 Million cell updates/sec

Title: US-10-720-424B-1

Perfect score: 29  
Sequence: 1 gatgctgatatggtacacaggatttgg 29

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_hic:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est7:  
9: gb\_gss1:  
10: gb\_gss2:  
11: gb\_gss3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.2	73.1	601	BI505309	BI170020B
2	21	72.4	687	CM611284	CM611284 OA_ABA015
3	21	72.4	738	AG537642	AG537642 Mus muscu
4	21	72.4	810	C2694085	C2694085 OC_Ha000
5	20.6	71.0	358	AL836877	AL836877 AL836877
6	20.6	71.0	370	AL836861	AL836861 AL836861
7	20.6	71.0	465	AZ159603	AZ159603 SP_0064_A
8	20.6	71.0	605	FR0037014	AL124517 Fugu rubr
9	20.6	71.0	770	BJ148396	BJ148396 BJ148396
10	20.6	71.0	776	BE277163	BE277163 601178502
11	20.4	70.3	250	AI020455	AI020455 ub26g05.r
12	20.4	70.3	327	AA210582	AA210582 mu71a03.r
13	20.4	70.3	490	BE147434	BE147434 BX31g01.x
14	20.4	70.3	528	EX513029	EX513029 EX513029
15	20.2	69.7	1020	CL056918	CL056918 CH216-B3P
16	20	69.0	137	AZ693668	AZ693668 AST-2HLB5
17	20	69.0	215	AW273632	AW273632 xv67h03.x
18	20	69.0	219	F04754	F04754 HSCZMG022.n
19	20	69.0	258	AW900192	AW900192 CMO-NN100
20	20	69.0	282	Z39966	Z39966 HSCIN042.n
21	20	69.0	325	CV376112	CV376112 PM3-SN001
22	20	69.0	353	AW207569	AW207569 UI-H-B11-

23	20	69.0	353	9	AQ357418	AQ357418 CITBI-E1-
24	20	69.0	356	5	BX115022	BX115022 BX115022
25	20	69.0	371	1	AI609876	AI609876 tt83e01.x
26	20	69.0	380	6	CF017665	CF017665 QBM2b09.x
27	20	69.0	380	6	CF017813	CF017813 QBM4a04.x
28	20	69.0	394	1	AA578113	AA578113 n129a01.8
29	20	69.0	430	9	AQ093787	AQ093787 HS_3023.B
30	20	69.0	443	9	AQ334764	AQ334764 HS_5009.B
31	20	69.0	489	9	AQ357438	AQ357438 CITBI-E1-
32	20	69.0	510	9	CE148431	CE148431 tigr-g88-
33	20	69.0	526	6	CD307313	CD307313 strPu691.
34	20	69.0	562	2	BF970237	BF970237 602273477
35	20	69.0	614	8	DN485400	DN485400 N001G08.3
36	20	69.0	703	5	BU685954	BU685954 UI-CF-DU1
37	20	69.0	746	7	CK351524	CK351524 tggfha39D
38	20	69.0	747	2	BE730479	BE730479 601562994
39	20	69.0	811	10	CM750547	CM750547 Op_Ba006
40	20	69.0	834	7	CO087160	CO087160 GR_Ea05H
41	20	69.0	888	3	BQ223384	BQ223384 AGENCOURT
42	20	69.0	1494	4	AK042726	AK042726 Mus muscu
43	19.8	68.3	554	9	CE113095	CE113095 tigr-g88-
44	19.8	68.3	649	8	DR532869	DR532869 WS02739.C
45	19.8	68.3	786	10	DU075702	DU075702 80192.Tom

#### ALIGNMENTS

RESULT 1  
BI505309

LOCUS  
DEFINITION

BI505309 601 bp mRNA linear EST 08-APR-2002  
BI170020BI0F08.5 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera cDNA clone BB170020BI0F08 5', mRNA sequence.

ACCESSION  
VERSION

BI505309.1 GI:15355683

KEYWORDS  
SOURCE

Apis mellifera (honey bee)  
Apis mellifera

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea; Apidae; Apis.

REFERENCE  
AUTHORS

Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L., Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.

TITLE

Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee

JOURNAL  
PUBMED

Genome Res. 12 (4), 555-566 (2002)  
11932240

COMMENT

Contact: Gene E. Robinson  
Department of Entomology  
University of Illinois  
505 S. Goodwin Ave., Urbana, IL 61801, USA  
Tel: 217 265 0309  
Fax: 217 244 3499

Email: generobi@life.uiuc.edu

This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.

PCR Primers

FORWARD: TAATACGACTCATATAGGG

BACKWARD: ATTAACCCCTCACTAAG

Plate: BI170020BI0 row: F column: 08

Seq primer: ACCGGTAACATTTTCACACAGGA

High quality sequence stop: 601.

Location/Qualifiers

1..601

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/mol\_type="mRNA"

/strain="mixed strains of European bees, predominantly

A.m. ligustica"

/db\_xref="taxon:7460"

/clone="BB170020BI0F08"

FEATURES  
source



ACCESSION C2694085  
 VERSION C2694085.1 GI:71093233  
 KEYWORDS GSS.  
 SOURCE Oryza coarctata (Porteresia coarctata)  
 ORGANISM Oryza coarctata  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoidae; Oryzeae; Oryza.  
 REFERENCE 1 (bases 1 to 810)  
 AUTHORS Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,  
 Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and  
 Wing,R.  
 TITLE OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute  
 JOURNAL Unpublished (2005)  
 COMMENT Contact: Rod A. Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: rwing@genome.arizona.edu  
 PCR Primers  
 FORWARD: TAA TAC GAC TCA CTA TAG GG  
 BACKWARD: CAC TCA TTA GGC ACC CCA  
 Plate: 0006 Row: L Column: 20  
 Seq primer: CAC TCA TTA GGC ACC CCA  
 Class: BAC ends.  
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 /clone\_lib="OC\_Ba"  
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 Best Local Similarity 82.8%; Pred.No. 3.3e+02;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 GATGGTGATGATGATGATGATGATGATGATG 29  
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 Db 234 GATGGTGATGATGATGATGATGATGATGATG 262  
 RESULT 5  
 AL836877  
 LOCUS AL836877 358 bp mRNA linear EST 27-FEB-2004  
 DEFINITION AL836877 EFRe Takifugu rubripes cDNA clone EFRe040apcK8, mRNA  
 sequence.  
 ACCESSION AL836877  
 VERSION AL836877.1 GI:21878839  
 KEYWORDS EST.  
 SOURCE Takifugu rubripes (Fugu rubripes)  
 ORGANISM Takifugu rubripes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 Tetraodontidae; Tetraodontidae; Takifugu.  
 REFERENCE 1 (bases 1 to 358)  
 AUTHORS Clark,M.S., Edwards,Y.J., Peterson,D., Clifton,S.W., Thompson,A.J.,  
 Sasaki,M., Suzuki,Y., Kikuchi,K., Watabe,S., Kawakami,K.,  
 Sugano,S., Elgar,G. and Johnson,S.L.  
 Fugu ESTs: new resources for transcription analysis and genome  
 annotation  
 TITLE Genome Res. 13 (12), 2747-2753 (2003)  
 JOURNAL Contact: Clark MS  
 COMMENT MRC Human Genome Mapping Project Resource Centre  
 Hinxton, Cambridge, CB10 1SB, UK  
 Email: biohelp@hgm.mrc.ac.uk  
 Vector: pBluescript II KS  
 PRIMER: KS  
 The clone can be obtained from www.hgm.mrc.ac.uk  
 Library created by Greg Elgar  
 MRC Human Genome Mapping Project Resource Centre, Hinxton,  
 Cambridge, CB10 1SB, UK  
 Library sequenced by Sarah Warner and Jim Hills  
 MRC Human Genome Mapping Project Resource Centre, Hinxton,  
 Cambridge, CB10 1SB, UK.  
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 /clone\_lib="EFRe"  
 /note="Vector: pBluescript II KS"

Email: biohelp@hgm.mrc.ac.uk  
 Email: biohelp@hgm.mrc.ac.uk  
 Vector: pBluescript II KS  
 V type: phagemid  
 PRIMER: KS  
 The clone can be obtained from www.hgm.mrc.ac.uk  
 Library created by Greg Elgar  
 MRC Human Genome Mapping Project Resource Centre, Hinxton,  
 Cambridge, CB10 1SB, UK  
 Library sequenced by Sarah Warner and Jim Hills  
 MRC Human Genome Mapping Project Resource Centre, Hinxton,  
 Cambridge, CB10 1SB, UK.  
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 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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 ||||| ||||| ||||| ||||| ||||| |||||  
 Db 222 GATGGTGATGATGATGATGATGATGATTT 248  
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 LOCUS AL836861 370 bp mRNA linear EST 27-FEB-2004  
 DEFINITION AL836861 EFRe Takifugu rubripes cDNA clone EFRe040apcK1, mRNA  
 sequence.  
 ACCESSION AL836861  
 VERSION AL836861.1 GI:21878823  
 KEYWORDS EST.  
 SOURCE Takifugu rubripes (Fugu rubripes)  
 ORGANISM Takifugu rubripes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 Tetraodontidae; Tetraodontidae; Takifugu.  
 REFERENCE 1 (bases 1 to 370)  
 AUTHORS Clark,M.S., Edwards,Y.J., Peterson,D., Clifton,S.W., Thompson,A.J.,  
 Sasaki,M., Suzuki,Y., Kikuchi,K., Watabe,S., Kawakami,K.,  
 Sugano,S., Elgar,G. and Johnson,S.L.  
 Fugu ESTs: new resources for transcription analysis and genome  
 annotation  
 TITLE Genome Res. 13 (12), 2747-2753 (2003)  
 JOURNAL Contact: Clark MS  
 COMMENT MRC Human Genome Mapping Project Resource Centre  
 Hinxton, Cambridge, CB10 1SB, UK  
 Email: biohelp@hgm.mrc.ac.uk  
 Vector: pBluescript II KS  
 V type: phagemid  
 PRIMER: KS  
 The clone can be obtained from www.hgm.mrc.ac.uk  
 Library created by Greg Elgar  
 MRC Human Genome Mapping Project Resource Centre, Hinxton,  
 Cambridge, CB10 1SB, UK  
 Library sequenced by Sarah Warner and Jim Hills  
 MRC Human Genome Mapping Project Resource Centre, Hinxton,  
 Cambridge, CB10 1SB, UK.  
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Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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    ||||| ||||| ||||| ||||| |||||
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RESULT 7
AZ159603/c
LOCUS
DEFINITION
SP_0064_A2_E10_T7A Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library Strongylocentrotus purpuratus
genomic clone Plate=64 Col=20 Row=1, genomic survey sequence.
ACCESSION
VERSION AZ159603
KEYWORDS
SOURCE
ORGANISM
Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinozoa; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE
1 (bases 1 to 465)
AUTHORS
Cameron,R.A., Mahirias G., Rast,J.P., Martinez,P., Biondi,T.R.,
Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T.,
Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H.
and Hood,L.
TITLE
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
JOURNAL
PROC. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
PUBMED
10920195
COMMENT
Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 64 row: 1 column: 20
Seq primer: T7
Class: BAC ends
High quality sequence stop: 465.
FEATURES
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            /notes="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
            DH10B"

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Best Local Similarity 82.1%; Pred. No. 4.6e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GATGGTGATATGGTAGATACAGGATTTG 28
    ||||| ||||| ||||| ||||| |||||
Db 56 GAGGGTGATATGATATATTCATGATTTG 29

RESULT 8
FR0037014
LOCUS
DEFINITION
SP_0064_A2_E10_T7A Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library Strongylocentrotus purpuratus
genomic clone Plate=64 Col=20 Row=1, genomic survey sequence.
ACCESSION
VERSION FR0037014
KEYWORDS
SOURCE
ORGANISM
Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinozoa; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE
1 (bases 1 to 605)
AUTHORS
Cameron,R.A., Mahirias G., Rast,J.P., Martinez,P., Biondi,T.R.,
Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T.,
Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H.
and Hood,L.
TITLE
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
JOURNAL
PROC. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
PUBMED
10920195
COMMENT
Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 64 row: 1 column: 20
Seq primer: T7
Class: BAC ends
High quality sequence stop: 605.
FEATURES
    source
    Location/Qualifiers
        1..605
            /organism="Takifugu rubripes"
            /mol_type="genomic DNA"
            /db_xref="taxon:31033"
            /clone="045I08B5"
            /clone_lib="cosmid 045I08"

ORIGIN
Query Match          71.0%; Score 20.6; DB 11; Length 605;
Best Local Similarity 85.2%; Pred. No. 4.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GATGGTGATATGGTAGATACAGGATTT 27
    ||||| ||||| ||||| ||||| |||||
Db 49 GATGGTGATCTGGTGACGAGGATTT 75

RESULT 9
BJ148396/c
LOCUS
DEFINITION
BJ148396 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1262d04 3', mRNA sequence.
ACCESSION
VERSION BJ148396
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 770)
AUTHORS
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE
A complementary view of the C.elegans genome
JOURNAL
Unpublished (2002)
COMMENT
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855

```

```

DEFINITION
Fugu rubripes GSS sequence, clone 045I08B5, genomic survey
sequence.
ACCESSION
VERSION AL124517.1 GI:6106132
KEYWORDS
SOURCE GSS; genome survey sequence.
ORGANISM Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Takifugu.
REFERENCE
1
AUTHORS Elgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,
Bouchireb,N., Cottage,A., Yeo,G.S., Umrana,Y., Williams,G. and
Brenner,S.
TITLE
Generation and analysis of 25 Mb of genomic DNA from the pufferfish
Fugu rubripes by sequence scanning
JOURNAL Genome Res. 9 (10), 960-971 (1999)
PUBMED 10523524
REFERENCE
2 (bases 1 to 605)
AUTHORS Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,
Umrana,Y., Williams,G. and Brenner,S.
TITLE
Direct Submission
JOURNAL Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
Centre, Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hgmrc.ac.uk
COMMENT
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
FEATURES
    source
    Location/Qualifiers
        1..605
            /organism="Takifugu rubripes"
            /mol_type="genomic DNA"
            /db_xref="taxon:31033"
            /clone="045I08B5"
            /clone_lib="cosmid 045I08"

ORIGIN
Query Match          71.0%; Score 20.6; DB 11; Length 605;
Best Local Similarity 85.2%; Pred. No. 4.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GATGGTGATATGGTAGATACAGGATTT 27
    ||||| ||||| ||||| ||||| |||||
Db 49 GATGGTGATCTGGTGACGAGGATTT 75

RESULT 9
BJ148396/c
LOCUS
DEFINITION
BJ148396 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1262d04 3', mRNA sequence.
ACCESSION
VERSION BJ148396
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 770)
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE
A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855

```

Email: tshini@genes.nig.ac.jp.

FEATURES  
source

1..770  
Location/Qualifiers  
/organism="Caenorhabditis elegans"  
/mol\_type="mRNA"  
/strain="N2"  
/db\_xref="taxon:6239"  
/clone="yk1262d04"  
/sex="hermaphrodite"  
/tissue\_type="whole animal"  
/dev\_stage="L1"  
/clone\_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"

## ORIGIN

Query Match 71.0%; Score 20.6; DB 3; Length 770;  
Best Local Similarity 85.2%; Pred. No. 4.9e+02;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATGGTGATATGGTAGATACAGGATTGG 28  
DB 558 ATGGGGATATGGTAGACAAAGGACTTG 532

## RESULT 10

BE277163 776 bp mRNA linear EST 13-JUL-2000  
LOCUS 601178502F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3050832 5',  
DEFINITION mRNA sequence.

ACCESSION BE277163

VERSION BE277163.1 GI:9152129

KEYWORDS EST.

SOURCE Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

## REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC/DCTD/PTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLC97 row: d column: 01

High quality sequence stop: 754.

## FEATURES

source

1..776

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3050832"

/tissue\_type="melanotic melanoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 20"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dt priming; Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGACACGAG(G). Size-selected &gt;500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 71.0%; Score 20.6; DB 2; Length 776;  
Best Local Similarity 85.2%; Pred. No. 4.9e+02;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGGTGATATGGTAGATACAGGATTGG 29  
DB 529 TGGTGTCTTTAGTAGACACAGGATTGG 555

## RESULT 11

AI020455/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS MUSCULUS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 250)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HHMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:901372

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 234.

Location/Qualifiers

1..250

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="CS7BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:1378904"

/sex="male"

/tissue\_type="Thymus"

/dev\_stage="4 weeks"

/lab\_host="DH10B"

/clone\_lib="Soares thymus 2NbMT"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was primed with a Not I oligo(dT) primer [5'

TGTACCAATCTGAAGTGGGCGCGCGGTTTTTTTTTTTTTTTTTTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. RNA

provided by Dr. Bertrand Jordan. Library went through two

rounds of normalization, and was constructed by Bento

Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 70.3%; Score 20.4; DB 1; Length 250;  
Best Local Similarity 95.5%; Pred. No. 5.2e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATGGTGATATGGTAGATACAGG 23

DB 96 ATGGTGATAGGTAGATACAGG 75

## RESULT 12

```

AA210582/c
LOCUS      AA210582      327 bp      mRNA      linear      EST 29-JAN-1997
DEFINITION mu71a03.r1 Soares mouse lymph node NBMLN Mus musculus cDNA clone
IMAGE:644812.5', mRNA sequence.
ACCESSION  AA210582
VERSION     AA210582.1  GI:1807829
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 327)
AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE      The WashU-HMI Mouse EST Project
JOURNAL    Unpublished (1996)
COMMENT    Contact: Marra M/Mouse EST Project
            WashU-HMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LML; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:396804
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 314.
FEATURES   source
            1..327
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:644812"
                /sex="male"
                /tissue_type="lymph node"
                /dev_stage="4 weeks"
                /lab_host="DH10B"
                /clone_lib="Soares mouse lymph node NBMLN"
                /notes="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia)
                with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
                1st strand cDNA was primed with a Not I - oligo(dT) primer
                [5'
                TGTTCACATCTGAGTGGAGCGCGCGATCTTTTITTTTTTTTTTTTTTTT
                3']; double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT7T3 vector. RNA
                provided by Dr. Bertrand Jordan. Library constructed and
                normalized by Bento Soares and M.Fatima Bonaldo."
ORIGIN
Query Match      70.3%; Score 20.4; DB 1; Length 327;
Best Local Similarity 95.5%; Pred. No. 5.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  ATGCGTATGCTAGATACAGG 23
        |||||
DB      126  ATGGTGATAGGGTAGATACAGG 105
        |||||

RESULT 13
BF147434
LOCUS      BF147434      490 bp      mRNA      linear      EST 26-OCT-2000
DEFINITION us31901.x1 Soares_NMEBA branchial arch Mus musculus cDNA clone
IMAGE:3168720.3', similar to TR:Q9VM41 Q9VM41 CGI5881 PROTEIN. ;,
mRNA sequence.
ACCESSION  BF147434
VERSION     BF147434.1  GI:11028829

```

```

KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 490)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Unpublished (1997)
TITLE      Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml
            MGI:1064180
            High quality sequence stop: 474.
FEATURES   Location/Qualifiers
            1..490
                /organism="Mus musculus"
                /mol_type="mRNA"
                /db_xref="taxon:10090"
                /clone="IMAGE:3168720"
                /tissue_type="branchial arches"
                /dev_stage="embryo, 10.5 dpc"
                /lab_host="DH10B (phage resistant)"
                /clone_lib="Soares NMEBA branchial arch"
                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA
                was primed with a Not I - oligo(dT) primer [5'
                TGTTCACATCTGAGTGGAGCGCGCGATCTTTTITTTTTTTTTTTTTTTT
                3']; double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not
                I and Eco RI sites of the modified pT7T3 vector. Library
                constructed and normalized by Bento Soares and M.Fatima
                Bonaldo."
ORIGIN
Query Match      70.3%; Score 20.4; DB 2; Length 490;
Best Local Similarity 95.5%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  ATGCGTATGCTAGATACAGG 23
        |||||
DB      427  ATGGTGATAGGGTAGATACAGG 448
        |||||

RESULT 14
BX513029/c
LOCUS      BX513029      528 bp      mRNA      linear      EST 25-JUN-2003
DEFINITION BX513029 Soares mouse lymph node NBMLN Mus musculus cDNA clone
IMAGE:952J0565 ; IMAGE:644812, mRNA sequence.
ACCESSION  BX513029
VERSION     BX513029.1  GI:32244756
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 528)
AUTHORS    Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D.
            and Korn,B.
TITLE      Mouse Unigeneset - RZPD2
JOURNAL    Unpublished (2003)
COMMENT    Contact: Ina Rolfe
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

```

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD: IMAGp952J0565.  
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;  
Mouse UniGeneSet - RZPD2 (RZPDLIB No.981)  
[http://www.rzpd.de/CloneCards/cgi-  
bin/showlib.pl.cgi?response=libNo-981](http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi?response=libNo-981) Contact: Ina Ro-  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
[www.rzpd.de](http://www.rzpd.de)

This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
T7, Primer sequence: TAATACGACTCACTATAGGG.

**FEATURES**  
**SOURCE**

```

location/qualifiers
1. 528
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="IMAGE955J0365 ; IMAGE:644812"
/sex="male"
/tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DH103"

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/cloneLib="Soares mouse lymph node NbMLN"  
 /note="Organ: lymph node; Vector: pT73D-Pac (Pharmacia)  
 with a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
 1st strand cDNA was primed with a Not I - oligo(dT) primer  
 [5,

15' TGTACCAATCTCGAAGTGGGAGCGCCGCATACTTTTTTTTTTTTTTTTTTTT

3'; double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fátima Bonaldo."

## ORIGIN

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Query Match          70.3%; Score 20.4; DB 5; Length 528;
Best Local Similarity 95.5%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 2 ATGGTGATATGGTAGATACAGG 23  
|||||  
Db 127 ATGGTGATAGGGTAGATACAGG 10

RESULT 15  
CL056918/c

CL056918 · 1020 bp DNA linear GSS 31-DEC-2003  
CH216-83P3\_RM1.1 CH216 *Xenopus tropicalis* genomic clone CH216-83P3,  
genomic survey sequence.

genome survey sequences  
 CL056918  
 CL056918.1 GI:40512831  
 GSS  
 ACCESSION  
 VERSION  
 KEYWORDS

ACQUAINTANCE	SOURCE	ORGANISM	DESCRIPTION
1	Xenopus tropicalis (western clawed frog)	Xenopus tropicalis	1.000000
2	Xenopus tropicalis (western clawed frog)	Xenopus tropicalis	1.000000

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.

REFERENCE  
1 (bases 1 to 1020)  
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,  
Mardis, E. and Wilson, R.

**TITLE** A physical map of the xenopus tropicalis genome  
**JOURNAL** Unpublished (2003)

COMMENT  
Contact: Richard K Wilson  
Genome Sequencing Center

Genome Sequencing Center  
Washington University School of Medicine  
Email: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)

Insert Length: 175000 Std Error: 0.00  
Seq primer: RM1 TACGACTCACTATAGGAGA

Class: BAC ends

High quality sequence start: 54

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FEATURES
  source
    Location/Qualifiers
      High quality sequence stop: 551.
      1. .1020

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1. 20210601
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clones="CH216-83P3"
/sex="male"
/cell_lines="Stock 248 F7A2, in"
/clone_libs="CH216"
/note="Vector: pTARBAC2.1; CHO
BAC library"

```

## ORIGIN

Query Match	59.7%	Score 20.2;	DB 10;	Length 1020;
Best Local Similarity	88.0%	Pred. No. 7.6e+02;		
Matches 22;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy 3	TCGTGATATGGTAGATACAGGATTT	27		
Db 844	TCGTGATTTGGTAGATAAGGGATTT	820		

Search completed: March 5, 2006, 23:57:58  
Job time : 3173 secs

**This Page Blank (uspto)**



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 19:08:04 ; Search time 80.5 Seconds  
(without alignments)  
640.364 Million cell updates/sec

Title: US-10-720-424B-1

Perfect score: 29  
Sequence: 1 gatggtgatggtgtagacaggttgg 29

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25.8	89.0	38	2	US-08-316-293-53
2	25.8	89.0	386	3	US-09-319-056B-4
3	25.8	89.0	386	3	US-09-319-056B-6
4	25.8	89.0	1524	2	US-08-409-122-1
5	25.8	89.0	1524	2	US-08-408-669-1
6	25.8	89.0	1524	3	US-08-913-644-1
7	24.2	83.4	410	3	US-09-000-266-7
8	24.2	83.4	410	3	US-09-000-266-9
9	24.2	83.4	410	3	US-09-628-099-7
10	24.2	83.4	410	3	US-09-628-099-9
11	24.2	83.4	410	3	US-10-056-360-7
12	24.2	83.4	410	3	US-10-056-360-9
13	24.2	83.4	410	3	US-10-056-359-7
14	24.2	83.4	410	3	US-10-056-359-9
15	24.2	83.4	1494	3	US-09-413-611A-5
16	24.2	83.4	1500	3	US-09-413-611A-7
17	24.2	83.4	1517	2	US-08-032-869A-2
18	24.2	83.4	1517	2	US-08-472-673-2
19	24.2	83.4	1517	2	US-08-475-782-2
20	24.2	83.4	1517	2	US-08-472-678-2
21	24.2	83.4	1517	2	US-08-484-503-2
22	24.2	83.4	1518	3	US-08-944-368A-1
23	24.2	83.4	1518	3	US-09-820-764-1
24	24.2	83.4	1518	3	US-09-986-118A-1

25	24.2	83.4	1518	3	US-09-824-017-1	Sequence 1, Appl
26	22.6	77.9	125	2	US-08-710-082-5	Sequence 5, Appl
27	22.6	77.9	125	2	US-08-710-082-20	Sequence 20, Appl
28	22.6	77.9	125	3	US-08-913-462-5	Sequence 5, Appl
29	22.6	77.9	125	3	US-08-913-462-20	Sequence 20, Appl
30	22.6	77.9	125	3	US-09-624-482-5	Sequence 5, Appl
31	22.6	77.9	125	3	US-09-624-482-20	Sequence 20, Appl
32	22.6	77.9	661	3	US-08-578-634C-3	Sequence 3, Appl
33	22.6	77.9	661	3	US-09-430-010-3	Sequence 3, Appl
34	22.6	77.9	662	3	US-08-578-634C-6	Sequence 6, Appl
35	22.6	77.9	662	3	US-09-430-010-6	Sequence 6, Appl
36	22.6	77.9	668	3	US-08-578-634C-2	Sequence 2, Appl
37	22.6	77.9	668	3	US-09-430-010-2	Sequence 2, Appl
38	22.6	77.9	1059	2	US-08-815-667-11	Sequence 11, Appl
39	22.6	77.9	1484	3	US-09-210-168-2	Sequence 2, Appl
40	22.6	77.9	1517	2	US-08-032-869A-1	Sequence 1, Appl
41	22.6	77.9	1517	2	US-08-472-673-1	Sequence 1, Appl
42	22.6	77.9	1517	2	US-08-475-782-1	Sequence 1, Appl
43	22.6	77.9	1517	2	US-08-472-678-1	Sequence 1, Appl
44	22.6	77.9	1517	2	US-08-484-503-1	Sequence 1, Appl
45	22.6	77.9	1518	2	US-08-815-667-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1  
US-08-316-293-53  
; Sequence 53, Application US/08316293  
; Patent No. 5484699  
; GENERAL INFORMATION:  
; APPLICANT: ABBOTT LABORATORIES  
; APPLICANT: Stanley R. Bouma  
; APPLICANT: Thomas G. Laffler  
; APPLICANT: Ronald L. Marshall  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES USEFUL AS  
; TITLE OF INVENTION: TYPE-SPECIFIC PROBES, PCR PRIMERS AND LCR PROBES  
; TITLE OF INVENTION: FOR THE AMPLIFICATION AND DETECTION OF HUMAN  
; TITLE OF INVENTION: PAPILLOMA VIRUS, AND RELATED KITS AND METHODS.  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: One Abbott Park Road  
; CITY: Abbott Park  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/316,293  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/965,665  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas D. Brinard  
; REGISTRATION NUMBER: 32,459  
; REFERENCE/DOCKET NUMBER: 4853 US.P1  
; TELEPHONE: (708) 937-4884  
; TELEFAX: (708) 937-9556  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)

US-08-316-293-53

Query Match 89.0%; Score 25.8; DB 2; Length 38;  
Best Local Similarity 93.1%; Pred. No. 0.12;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GATGGTATGTTAGTACAGGATTGG 29  
Db 1 GATGGTATGTTAGTACAGGATTGG 29

RESULT 2

US-09-319-056B-4  
; Sequence 4, Application US/09319056B  
; Patent No. 6413522  
; GENERAL INFORMATION:  
; APPLICANT: de Villiers-zur Hausen, Ethel-Michele  
; APPLICANT: zur Hausen, Harald  
; APPLICANT: Laverigne, Donna  
; APPLICANT: Benton, Claire  
; TITLE OF INVENTION: PAPILLOMA VIRUSES, PRODUCTS FOR THE  
; TITLE OF INVENTION: DETECTION THEREOF AS WELL AS FOR TREATING DISEASES CAUSED BY  
; TITLE OF INVENTION: THEM  
; FILE REFERENCE: 8484-0086-999  
; CURRENT APPLICATION NUMBER: US/09/319,056B  
; CURRENT FILING DATE: 1999-08-05  
; PRIOR APPLICATION NUMBER: PCT/DE97/02659  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: DE 196 48 962.8  
; PRIOR FILING DATE: 1996-11-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 386  
; TYPE: DNA  
; ORGANISM: Papilloma virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(384)  
US-09-319-056B-4

Query Match 89.0%; Score 25.8; DB 3; Length 386;  
Best Local Similarity 93.1%; Pred. No. 0.15;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GATGGTATGTTAGTACAGGATTGG 29  
Db 7 GATGGTATGTTAGTACAGGATTGG 35

RESULT 3

US-09-319-056B-6/c  
; Sequence 6, Application US/09319056B  
; Patent No. 6413522  
; GENERAL INFORMATION:  
; APPLICANT: de Villiers-zur Hausen, Ethel-Michele  
; APPLICANT: zur Hausen, Harald  
; APPLICANT: Laverigne, Donna  
; APPLICANT: Benton, Claire  
; TITLE OF INVENTION: PAPILLOMA VIRUSES, PRODUCTS FOR THE  
; TITLE OF INVENTION: DETECTION THEREOF AS WELL AS FOR TREATING DISEASES CAUSED BY  
; TITLE OF INVENTION: THEM  
; FILE REFERENCE: 8484-0086-999  
; CURRENT APPLICATION NUMBER: US/09/319,056B  
; CURRENT FILING DATE: 1999-08-05  
; PRIOR APPLICATION NUMBER: PCT/DE97/02659  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: DE 196 48 962.8  
; PRIOR FILING DATE: 1996-11-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 386

; TYPE: DNA  
; ORGANISM: Papilloma virus  
US-09-319-056B-6

Query Match 89.0%; Score 25.8; DB 3; Length 386;  
Best Local Similarity 93.1%; Pred. No. 0.15;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GATGGTATGTTAGTACAGGATTGG 29  
Db 380 GATGGTATGTTAGTACAGGATTGG 352

RESULT 4

US-08-409-122-1  
; Sequence 1, Application US/08409122  
; Patent No. 5820870  
; GENERAL INFORMATION:  
; APPLICANT: JOYCE, JAMES G.  
; APPLICANT: GEORGE, HUGH A.  
; APPLICANT: HOFMANN, KATHRYN J.  
; APPLICANT: JANSEN, KATHRIN U.  
; APPLICANT: NEPPER, MICHAEL P.  
; TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18 VACCINE  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC.  
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
; CITY: RAHWAY  
; STATE: NJ  
; COUNTRY: US  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/409,122  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/408,669  
; FILING DATE: 22-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARTY, CHRISTINE E  
; REGISTRATION NUMBER: 36,099  
; REFERENCE/DOCKET NUMBER: 19425  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 908-594-6734  
; TELEFAX: 908-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1524 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
US-08-409-122-1

Query Match 89.0%; Score 25.8; DB 2; Length 1524;  
Best Local Similarity 93.1%; Pred. No. 0.18;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GATGGTATGTTAGTACAGGATTGG 29  
Db 589 GATGGTATGTTAGTACAGGATTGG 617

RESULT 5  
US-08-408-669-1  
; Sequence 1, Application US/08408669  
; Patent No. 5840306  
; GENERAL INFORMATION:  
; APPLICANT: HOPMANN, KATHRYN J.  
; APPLICANT: JANSEN, KATHRIN U.  
; APPLICANT: NEEPER, MICHAEL P.  
; TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC.  
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
; CITY: RAHWAY  
; STATE: NJ  
; COUNTRY: US  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,669  
; FILING DATE: 22-MAR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARTY, CHRISTINE E  
; REGISTRATION NUMBER: 36,099  
; REFERENCE/DOCKET NUMBER: 19424  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 908-594-6734  
; TELEFAX: 908-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1524 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
US-08-408-669-1

Query Match 89.0%; Score 25.8; DB 2; Length 1524;  
Best Local Similarity 93.1%; Pred. No. 0.18; Mismatches 0; Gaps 0;  
Matches 27; Conservative 0; Indels 2; Indels 0; Gaps 0;  
QY 1 GATGGTGATGGTAGATACAGGATTGG 29  
|||||  
Db 589 GATGGTGATGGTAGATACAGGATTGG 617

RESULT 6  
US-08-913-644-1  
; Sequence 1, Application US/08913644  
; Patent No. 6908615  
; GENERAL INFORMATION:  
; APPLICANT: Hofmann, Kathryn J.  
; APPLICANT: Jansen, Kathrin U.  
; APPLICANT: Neeper, Michael P.  
; TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE  
; TITLE OF INVENTION: 18  
; FILE REFERENCE: 19424PC  
; CURRENT APPLICATION NUMBER: US/08/913,644  
; CURRENT FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: PCT/US96/03649  
; PRIOR FILING DATE: 1996-03-18  
; PRIOR APPLICATION NUMBER: 08/408,669  
; PRIOR FILING DATE: 1995-03-22  
; PRIOR APPLICATION NUMBER: 08/409,122  
; PRIOR FILING DATE: 1995-03-22  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1524  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HPV18 L1 Consensus Sequence  
US-08-913-644-1

Query Match 89.0%; Score 25.8; DB 3; Length 1524;  
Best Local Similarity 93.1%; Pred. No. 0.18; Mismatches 0; Gaps 0;  
Matches 27; Conservative 0; Indels 2; Indels 0; Gaps 0;  
QY 1 GATGGTGATGGTAGATACAGGATTGG 29  
|||||  
Db 589 GATGGTGATGGTAGATACAGGATTGG 617

RESULT 7  
US-09-000-266-7  
; Sequence 7, Application US/09000266A  
; Patent No. 6322795  
; GENERAL INFORMATION:  
; APPLICANT: Shamanin, Vladimir  
; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele  
; APPLICANT: Zur Hausen, Harald  
; TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING  
; TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES  
; FILE REFERENCE: 8484-0037-999  
; CURRENT APPLICATION NUMBER: US/09/000,266A  
; CURRENT FILING DATE: 1998-10-19  
; EARLIER APPLICATION NUMBER: PCT/DE96/01369  
; EARLIER FILING DATE: 1996-07-19  
; EARLIER APPLICATION NUMBER: DE P 195 26 386.3  
; EARLIER FILING DATE: 1995-07-19  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 410  
; TYPE: DNA  
; ORGANISM: Papilloma virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(408)  
US-09-000-266-7

Query Match 83.4%; Score 24.2; DB 3; Length 410;  
Best Local Similarity 89.7%; Pred. No. 0.71; Mismatches 3; Indels 0; Gaps 0;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GATGGTGATGGTAGATACAGGATTGG 29  
|||||  
Db 13 GATGGTGATGGTAGATACAGGATTGG 41

RESULT 8  
US-09-000-266-9/c  
; Sequence 9, Application US/09000266A  
; Patent No. 6322795  
; GENERAL INFORMATION:  
; APPLICANT: Shamanin, Vladimir  
; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele  
; APPLICANT: Zur Hausen, Harald  
; TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING  
; TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES  
; FILE REFERENCE: 8484-0037-999

; CURRENT APPLICATION NUMBER: US/09/000,266A  
; CURRENT FILING DATE: 1998-10-19  
; EARLIER APPLICATION NUMBER: PCT/DE96/01369  
; EARLIER FILING DATE: 1996-07-19  
; EARLIER APPLICATION NUMBER: DE P 195 26 386.3  
; EARLIER FILING DATE: 1995-07-19  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 410  
; TYPE: DNA  
; ORGANISM: Papilloma virus  
US-09-000-266-9

Query Match 83.4%; Score 24.2; DB 3; Length 410;  
Best Local Similarity 89.7%; Pred. No. 0.71;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTATGCTAGATACAGGATTGG 29  
|||||  
DB 398 GATGGTATGCTAGATACAGGATTGG 370

## RESULT 9

US-09-628-099-7  
; Sequence 7, Application US/09628099

; Patent No. 6368832

; GENERAL INFORMATION:

; APPLICANT: Shamanin, Vladimir

; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele

; APPLICANT: Zur Hausen, Harald

; TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING

; FILE REFERENCE: 8484-0037-999

; CURRENT APPLICATION NUMBER: US/09/628,099

; CURRENT FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 09/000,266

; PRIOR FILING DATE: 1998-10-19

; PRIOR APPLICATION NUMBER: DE P 195 26 386.3

; PRIOR FILING DATE: 1995-07-19

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 410

; TYPE: DNA

; ORGANISM: Papilloma virus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(408)

US-09-628-099-7

Query Match 83.4%; Score 24.2; DB 3; Length 410;  
Best Local Similarity 89.7%; Pred. No. 0.71;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTATGCTAGATACAGGATTGG 29  
|||||  
DB 13 GATGGTATGCTAGATACAGGATTGG 41

## RESULT 10

US-09-628-099-9/c

; Sequence 9, Application US/09628099

; Patent No. 6368832

; GENERAL INFORMATION:

; APPLICANT: Shamanin, Vladimir

; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele

; APPLICANT: Zur Hausen, Harald

; TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING

; FILE REFERENCE: 8484-0037-999

; CURRENT APPLICATION NUMBER: US/09/628,099

; CURRENT FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 09/000,266  
; PRIOR FILING DATE: 1998-10-19  
; PRIOR APPLICATION NUMBER: DE P 195 26 386.3  
; PRIOR FILING DATE: 1995-07-19  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 410  
; TYPE: DNA  
; ORGANISM: Papilloma virus  
US-09-628-099-9

Query Match 83.4%; Score 24.2; DB 3; Length 410;  
Best Local Similarity 89.7%; Pred. No. 0.71;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTATGCTAGATACAGGATTGG 29  
|||||  
DB 398 GATGGTATGCTAGATACAGGATTGG 370

## RESULT 11

US-10-056-360-7

; Sequence 7, Application US/10056360

; Patent No. 6555345

; GENERAL INFORMATION:

; APPLICANT: Shamanin, Vladimir

; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele

; APPLICANT: Zur Hausen, Harald

; TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING

; FILE REFERENCE: 8484-0037-999

; CURRENT APPLICATION NUMBER: US/10/056,360

; CURRENT FILING DATE: 2000-01-23

; PRIOR APPLICATION NUMBER: US/09/628,099

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 09/000,266

; PRIOR FILING DATE: 1998-10-19

; PRIOR APPLICATION NUMBER: DE P 195 26 386.3

; PRIOR FILING DATE: 1995-07-19

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 410

; TYPE: DNA

; ORGANISM: Papilloma virus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(408)

US-10-056-360-7

Query Match 83.4%; Score 24.2; DB 3; Length 410;  
Best Local Similarity 89.7%; Pred. No. 0.71;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTATGCTAGATACAGGATTGG 29  
|||||  
DB 13 GATGGTATGCTAGATACAGGATTGG 41

## RESULT 12

US-10-056-360-9/c

; Sequence 9, Application US/10056360

; Patent No. 6555345

; GENERAL INFORMATION:

; APPLICANT: Shamanin, Vladimir

; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele

; APPLICANT: Zur Hausen, Harald

; TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING

; FILE REFERENCE: 8484-0037-999

; CURRENT APPLICATION NUMBER: US/10/056,360

; CURRENT FILING DATE: 2000-01-23

; PRIOR APPLICATION NUMBER: US/09/628,099  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 09/000,266  
; PRIOR FILING DATE: 1998-10-19  
; PRIOR APPLICATION NUMBER: DE P 195 26 386.3  
; PRIOR FILING DATE: 1995-07-19  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 410  
; TYPE: DNA  
; ORGANISM: Papilloma virus  
US-10-056-360-9

Query Match 83.4%; Score 24.2; DB 3; Length 410;  
Best Local Similarity 89.7%; Pred. No. 0.71;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTATGTTAGTACAGGATTGG 29  
DB 398 GATGGTATGTTAGTACAGGATTGG 370

RESULT 13  
US-10-056-359-7  
; Sequence 7, Application US/10056359  
; Patent No. 6562597  
; GENERAL INFORMATION:  
; APPLICANT: Shamanin, Vladimir  
; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele  
; APPLICANT: Zur Hausen, Harald  
; TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING  
; TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES  
; FILE REFERENCE: 8484-0037-999  
; CURRENT APPLICATION NUMBER: US/10/056,359  
; CURRENT FILING DATE: 2002-01-23  
; PRIOR APPLICATION NUMBER: US/09/628,099  
; PRIOR FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: 09/000,266  
; PRIOR FILING DATE: 1998-10-19  
; PRIOR APPLICATION NUMBER: DE P 195 26 386.3  
; PRIOR FILING DATE: 1995-07-19  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 410  
; TYPE: DNA  
; ORGANISM: Papilloma virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(408)  
US-10-056-359-7

Query Match 83.4%; Score 24.2; DB 3; Length 410;  
Best Local Similarity 89.7%; Pred. No. 0.71;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTATGTTAGTACAGGATTGG 29  
DB 13 GATGGTATGTTAGTACAGGATTGG 41

RESULT 14  
US-10-056-359-9/c  
; Sequence 9, Application US/10056359  
; Patent No. 6562597  
; GENERAL INFORMATION:  
; APPLICANT: Shamanin, Vladimir  
; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele  
; APPLICANT: Zur Hausen, Harald  
; TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING  
; TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES  
; FILE REFERENCE: 8484-0037-999

; CURRENT APPLICATION NUMBER: US/10/056,359  
; CURRENT FILING DATE: 2002-01-23  
; PRIOR APPLICATION NUMBER: US/09/628,099  
; PRIOR FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: 09/000,266  
; PRIOR FILING DATE: 1998-10-19  
; PRIOR APPLICATION NUMBER: DE P 195 26 386.3  
; PRIOR FILING DATE: 1995-07-19  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 410  
; TYPE: DNA  
; ORGANISM: Papilloma virus  
US-10-056-359-9

Query Match 83.4%; Score 24.2; DB 3; Length 410;  
Best Local Similarity 89.7%; Pred. No. 0.71;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTATGTTAGTACAGGATTGG 29  
DB 398 GATGGTATGTTAGTACAGGATTGG 370

RESULT 15  
US-09-413-611A-5  
; Sequence 5, Application US/09413611A  
; Patent No. 6380364  
; GENERAL INFORMATION:  
; APPLICANT: Mueller, Martin  
; APPLICANT: Kast, Wjbe  
; APPLICANT: Nieland, John  
; APPLICANT: Velders, Markwin  
; TITLE OF INVENTION: Chimeric Biotin-Binding Papillomavirus Protein  
; FILE REFERENCE: 202325  
; CURRENT APPLICATION NUMBER: US/09/413,611A  
; CURRENT FILING DATE: 1999-10-06  
; PRIOR APPLICATION NUMBER: US 60/109,510  
; PRIOR FILING DATE: 1998-11-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1494  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: biotin-binding  
; OTHER INFORMATION: papillomavirus protein 168  
; NAME/KEY: CDS  
; LOCATION: (1)...(1491)  
US-09-413-611A-5

Query Match 83.4%; Score 24.2; DB 3; Length 1494;  
Best Local Similarity 89.7%; Pred. No. 0.81;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTATGTTAGTACAGGATTGG 29  
DB 589 GATGGTATGTTAGTACAGGATTGG 617

Search completed: March 5, 2006, 19:13:35  
Job time : 81.5 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:00:24 ; Search time 361 Seconds  
(without alignments)  
664.299 Million cell updates/sec

Title: US-10-720-424B-1  
Perfect score: 29  
Sequence: 1 gatggtgatgtgtagacaggatttgg 29

Scoring table: IDENTITY NUC  
Gap 10\_0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA\_Main:  
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3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
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7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	29	US-10-720-424B-1	Sequence 1, Appli
2	25.8	89.0	1421	7 US-10-433-091-1	Sequence 1, Appli
3	24.2	83.4	410	5 US-10-056-359-7	Sequence 7, Appli
4	24.2	83.4	410	5 US-10-056-359-9	Sequence 9, Appli
5	24.2	83.4	410	5 US-10-056-360-7	Sequence 7, Appli
6	24.2	83.4	410	5 US-10-056-360-9	Sequence 9, Appli
7	24.2	83.4	1452	9 US-10-487-719-2	Sequence 2, Appli
8	24.2	83.4	1452	9 US-10-487-719-4	Sequence 4, Appli
9	24.2	83.4	1517	3 US-09-832-065-2	Sequence 2, Appli
10	24.2	83.4	1517	6 US-10-371-846-2	Sequence 2, Appli
11	24.2	83.4	1518	3 US-09-820-765-1	Sequence 1, Appli
12	24.2	83.4	1518	3 US-09-162-904A-1	Sequence 2, Appli
13	24.2	83.4	1518	3 US-09-162-904A-2	Sequence 2, Appli
14	24.2	83.4	1518	3 US-09-824-017-1	Sequence 1, Appli
15	24.2	83.4	1518	3 US-09-986-118A-1	Sequence 1, Appli
16	24.2	83.4	1518	6 US-10-367-095-11	Sequence 11, Appli
17	24.2	83.4	1518	7 US-10-368-046-11	Sequence 11, Appli
18	24.2	83.4	1518	7 US-10-654-129-1	Sequence 1, Appli
19	24.2	83.4	1518	7 US-10-367-367-11	Sequence 11, Appli
20	24.2	83.4	1518	8 US-10-042-526A-1	Sequence 1, Appli
21	24.2	83.4	1518	9 US-10-487-719-1	Sequence 1, Appli
22	24.2	83.4	1518	9 US-10-487-719-3	Sequence 3, Appli
23	24.2	83.4	1518	9 US-10-918-337-11	Sequence 11, Appli

24	24.2	83.4	1890	3	US-09-864-408A-8573	Sequence 8573, Ap
25	22.6	77.9	1404	8	US-10-475-203A-7	Sequence 7, Appli
26	22.6	77.9	1484	3	US-09-970-477-2	Sequence 2, Appli
27	22.6	77.9	1503	8	US-10-475-203A-3	Sequence 3, Appli
28	22.6	77.9	1517	3	US-09-832-065-1	Sequence 1, Appli
29	22.6	77.9	1517	6	US-10-371-846-1	Sequence 1, Appli
30	22.6	77.9	1518	6	US-10-367-095-12	Sequence 12, Appli
31	22.6	77.9	1518	7	US-10-368-046-12	Sequence 12, Appli
32	22.6	77.9	1518	7	US-10-367-367-12	Sequence 12, Appli
33	22.6	77.9	1518	9	US-10-918-337-12	Sequence 12, Appli
34	22.6	77.9	1596	9	US-10-367-057-115	Sequence 115, App
35	22.6	77.9	7804	9	US-10-494-800-2	Sequence 2, Appli
36	21.2	73.1	1849	5	US-10-112-178-1	Sequence 1, Appli
c 37	21	72.4	398	5	US-10-056-359-28	Sequence 28, Appli
c 38	21	72.4	398	5	US-10-056-359-30	Sequence 30, Appli
c 39	21	72.4	398	5	US-10-056-360-28	Sequence 28, Appli
c 40	21	72.4	398	5	US-10-056-360-30	Sequence 30, Appli
c 41	21	72.4	416	5	US-10-056-359-22	Sequence 22, Appli
c 42	21	72.4	416	5	US-10-056-359-24	Sequence 22, Appli
c 43	21	72.4	416	5	US-10-056-360-22	Sequence 22, Appli
c 44	21	72.4	416	5	US-10-056-360-24	Sequence 24, Appli
c 45	21	72.4	425	5	US-10-056-359-25	Sequence 25, Appli

## ALIGNMENTS

RESULT 1  
US-10-720-424B-1  
; Sequence 1, Application US/10720424B  
; Publication No. US20040248085A1  
; GENERAL INFORMATION:  
; APPLICANT: ALBIONED CO., LTD  
; APPLICANT: Lee, Sang-Wha  
; APPLICANT: Kim, Yeon-Soo  
; APPLICANT: Yu, Kang-Yeol  
; APPLICANT: Kim, Seung-Jo  
; APPLICANT: Cha, Kwang-Yul  
; APPLICANT: Ko, Jung-Jae  
; TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF  
; FILE REFERENCE: NET0018  
; CURRENT APPLICATION NUMBER: US/10/720,424B  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: KR10-2002-0075370  
; PRIOR FILING DATE: 2002-11-29  
; PRIOR APPLICATION NUMBER: KR10-2003-0053147  
; PRIOR FILING DATE: 2003-07-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Human Papillomavirus  
US-10-720-424B-1

Query Match 100.0%; Score 29; DB 8; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCTGATATGGTAGATACAGGATTGG 29  
Db 1 GATGCTGATATGGTAGATACAGGATTGG 29

RESULT 2  
US-10-433-091-1  
; Sequence 1, Application US/10433091  
; Publication No. US20040101533A1  
; GENERAL INFORMATION:  
; APPLICANT: MULLER, RAINER  
; APPLICANT: NIELAND, JOHN  
; APPLICANT: GABELSBERGER, JOSEF

```
; APPLICANT: HERBST, RUTH
; TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
; FILE REFERENCE: 037067/0115
; CURRENT APPLICATION NUMBER: US/10/433,091
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/14038
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 100 59 630.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1421
; TYPE: DNA
; ORGANISM: Human papillomavirus type 18
US-10-433-091-1

Query Match      89.0%; Score 25.8; DB 7; Length 1421;
Best Local Similarity 93.1%; Pred. No. 1.2;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGGTGATGCTAGATACAGATTGG 29
    |||||
Db 589 GATGGTGATGCTAGATGACTGGATGG 617
    |||||

RESULT 3
US-10-056-359-7
; Sequence 7, Application US/10056359
; Publication No. US20020110865A1
; GENERAL INFORMATION:
; APPLICANT: Shamanin, Vladimir
; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele
; TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
; FILE REFERENCE: 8484-0037-999
; CURRENT APPLICATION NUMBER: US/10/056,359
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US/09/628,099
; PRIOR FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/000,266
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: DE P 195 26 386.3
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 410
; TYPE: DNA
; ORGANISM: Papilloma virus
; NAME/KEY: CDS
; LOCATION: (1)...(408)
US-10-056-359-7

Query Match      83.4%; Score 24.2; DB 5; Length 410;
Best Local Similarity 89.7%; Pred. No. 4.4;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTGATGCTAGATACAGATTGG 29
    |||||
Db 13 GATGGTGATGCTAGATAGGATTGG 41
    |||||

RESULT 4
US-10-056-359-9/c
; Sequence 9, Application US/10056359
; Publication No. US20020110865A1
; GENERAL INFORMATION:
; APPLICANT: Shamanin, Vladimir
; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele
```

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; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
; FILE REFERENCE: 8484-0037-999
; CURRENT APPLICATION NUMBER: US/10/056,359
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US/09/628,099
; PRIOR FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/000,266
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: DE P 195 26 386.3
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 410
; TYPE: DNA
; ORGANISM: Papilloma virus
US-10-056-359-9

Query Match      83.4%; Score 24.2; DB 5; Length 410;
Best Local Similarity 89.7%; Pred. No. 4.4;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTGATGCTAGATACAGATTGG 29
    |||||
Db 398 GATGGTGATGCTAGATAGGATTGG 370
    |||||

RESULT 5
US-10-056-360-7
; Sequence 7, Application US/10056360
; Publication No. US20020110866A1
; GENERAL INFORMATION:
; APPLICANT: Shamanin, Vladimir
; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele
; TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
; FILE REFERENCE: 8484-0037-999
; CURRENT APPLICATION NUMBER: US/10/056,360
; PRIOR FILING DATE: 2000-01-23
; PRIOR APPLICATION NUMBER: US/09/628,099
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/000,266
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: DE P 195 26 386.3
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 410
; TYPE: DNA
; ORGANISM: Papilloma virus
; NAME/KEY: CDS
; LOCATION: (1)...(408)
US-10-056-360-7

Query Match      83.4%; Score 24.2; DB 5; Length 410;
Best Local Similarity 89.7%; Pred. No. 4.4;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTGATGCTAGATACAGATTGG 29
    |||||
Db 13 GATGGTGATGCTAGATAGGATTGG 41
    |||||

RESULT 6
US-10-056-360-9/c
; Sequence 9, Application US/10056360
; Publication No. US20020110866A1
; GENERAL INFORMATION:
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; APPLICANT: Shamanin, Vladimir
; APPLICANT: De Villiers-Zur Hausen, Ethel-Wichele
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
; TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
; FILE REFERENCE: 8484-0037-999
; CURRENT APPLICATION NUMBER: US/10/056,360
; CURRENT FILING DATE: 2000-01-23
; PRIOR APPLICATION NUMBER: US/09/628,099
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/000,266
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: DE P 195 26 386.3
; PRIOR FILING DATE: 1995-07-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 410
; TYPE: DNA
; ORGANISM: Papilloma virus
; US-10-056-360-9

Query Match      83.4%; Score 24.2; DB 5; Length 410;
Best Local Similarity 89.7%; Pred. No. 4.4;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTGATGCGGTAGATACAGGATTGG 29
   |||||
Db 398 GATGGTGATGCGGTAGATACAGGATTGG 370

RESULT 7
US-10-487-719-2
; Sequence 2, Application US/10487719
; Publication No. US20050090435A1
; GENERAL INFORMATION:
; APPLICANT: Varsani, Arvind
; APPLICANT: Tybicki, Edward
; APPLICANT: Williamson, Anna-Lise
; TITLE OF INVENTION: Pharmaceutical Compositions, and a Method of Preparing and
; TITLE OF INVENTION: Isolating Said Pharmaceutical Compositions, and Use of Said
; TITLE OF INVENTION: Pharmaceutical Compositions for Prophylactic Treatment of
; TITLE OF INVENTION: Lesions and Carcinomas
; FILE REFERENCE: 025455-116
; CURRENT APPLICATION NUMBER: US/10/487,719
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: PCT/IB02/03531
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: ZA 2001/7228
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: fragment of L1 gene
US-10-487-719-2

Query Match      83.4%; Score 24.2; DB 9; Length 1452;
Best Local Similarity 89.7%; Pred. No. 5.5;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTGATGCGGTAGATACAGGATTGG 29
   |||||
Db 589 GATGGTGATGCGGTAGATACAGGATTGG 617

RESULT 8
US-10-487-719-4
; Sequence 4, Application US/10487719
; Publication No. US20050090435A1
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; GENERAL INFORMATION:
; APPLICANT: Varsani, Arvind
; APPLICANT: Tybicki, Edward
; APPLICANT: Williamson, Anna-Lise
; TITLE OF INVENTION: Pharmaceutical Compositions, and a Method of Preparing and
; TITLE OF INVENTION: Isolating Said Pharmaceutical Compositions, and Use of Said
; TITLE OF INVENTION: Pharmaceutical Compositions for Prophylactic Treatment of
; TITLE OF INVENTION: Lesions and Carcinomas
; FILE REFERENCE: 025455-116
; CURRENT APPLICATION NUMBER: US/10/487,719
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: PCT/IB02/03531
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: ZA 2001/7228
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of L1 gene
US-10-487-719-4

Query Match      83.4%; Score 24.2; DB 9; Length 1452;
Best Local Similarity 89.7%; Pred. No. 5.5;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTGATGCGGTAGATACAGGATTGG 29
   |||||
Db 589 GATGGTGATGCGGTAGATACAGGATTGG 617

RESULT 9
US-09-832-065-2
; Sequence 2, Application US/09832065
; Publication No. US20030050439A1
; GENERAL INFORMATION:
; APPLICANT: Lowy, Douglas R.
; APPLICANT: Kirmbauer, Reinhard
; APPLICANT: Schiller, John T.
; TITLE OF INVENTION: SELF-ASSEMBLING RECOMBINANT
; TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/832,065
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/316,487
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirkpatrick Ph.D., Anita M.
; REGISTRATION NUMBER: 32,617
; REFERENCE/DOCKET NUMBER: NIH032.001CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 1517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1517
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-832-065-2

Query Match      83.4%; Score 24.2; DB 3; Length 1517;
Best Local Similarity 89.7%; Pred. No. 5.5;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTGATATGATAGATACAGGATTGG 29
Db 589 GATGGTGATATGATAGTACTGGCTTTGG 617

RESULT 10
US-10-371-846-2
; Sequence 2, Application US/10371846
; Publication No. US20030219873A1
; GENERAL INFORMATION:
; APPLICANT: Lowy, Douglas R.
; Kirnbauer, Reinhard
; Schiller, John T.
; TITLE OF INVENTION: SELF-ASSEMBLING RECOMBINANT
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/371,846
; FILING DATE: 21-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/032,869
; FILING DATE: 16-MAR-1993
; APPLICATION NUMBER: US 07/941,371
; FILING DATE: 03-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirkpatrick Ph.D., Anita M.
; REGISTRATION NUMBER: 32,617
; REFERENCE/DOCKET NUMBER: NIH032.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1517

;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-371-846-2

Query Match      83.4%; Score 24.2; DB 6; Length 1517;
Best Local Similarity 89.7%; Pred. No. 5.5;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTGATATGATAGATACAGGATTGG 29
Db 589 GATGGTGATATGATAGTACTGGCTTTGG 617

RESULT 11
US-09-820-765-1
; Sequence 1, Application US/09820765
; Publication No. US20020039584A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,765
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1518 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1515
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-820-765-1

Query Match      83.4%; Score 24.2; DB 3; Length 1518;
Best Local Similarity 89.7%; Pred. No. 5.5;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTGATATGATAGATACAGGATTGG 29
Db 589 GATGGTGATATGATAGTACTGGCTTTGG 617

RESULT 12
US-09-162-904A-1
; Sequence 1, Application US/09162904A
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RESULT 14  
US-09-824-017-1  
Sequence 1, Application US/09824017  
Publication No. US20020197668A1  
GENERAL INFORMATION:  
APPLICANT: BURGER, Alexander  
APPLICANT: HALLEK, Michael  
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
FORMULATIONS AND METHODS OF USE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/824,017  
FILING DATE: 03-APR-2001  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/026,896  
FILING DATE: 1998-02-20  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercok, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1518 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1515  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-824-017-1

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; ; ; ; ;
; TELEFAX: (202) 672-5399
; ; ; INFORMATION FOR SEQ ID NO: 1:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 1518 base pairs
; ; TYPE: nucleic acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; ; NAME/KEY: CDS
; ; LOCATION: 1..1515
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-09-824-017-1
;
; Query Match      83.4%;   Score 24.2; DB 3; Length 1518;
; Best Local Similarity 89.7%; Pred. No. 5.5;
; Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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; QY      1 GATGGTGATGTGATAGTACAGGATTGG 29
;         |||||||
; Db      589 GATGGTGATGTGTTGACTACTGTCCTTGG 617
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; RESULT 15
; US-09-886-118A-1
; Sequence 1, Application US/09986118A
; Publication No. US20030021806A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
;             HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.

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; COUNTRY: U.S.A.
; ZIP: 20007-Si09
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/986,118A
; FILING DATE: 07-No. US20030021806A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1518 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1515
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-986-118A-1

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Query Match      83.4%; Score 24.2; DB 3; Length 1518;
Best Local Similarity 89.7%; Pred. No. 5.5;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GATGGTGATATGGTAGATACAGGATTGG 29
      |||||
Db      589 GATGGTGATATGGTAGACTGCTTGG 617

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Job time : 362 secs

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2	24.2	83.4	1518	7 US-10-514-878A-4	Sequence 4, Appli
3	24.2	83.4	1518	7 US-10-514-878A-6	Sequence 6, Appli
4	24.2	83.4	1518	7 US-10-514-878A-8	Sequence 8, Appli
5	24.2	83.4	1518	7 US-10-514-878A-10	Sequence 10, Appli
6	24.2	83.4	1518	7 US-10-514-878A-12	Sequence 12, Appli
7	24.2	83.4	1518	12 US-11-179-478-1	Sequence 1, Appli
8	19.6	67.6	623	6 US-09-925-065A-809541	Sequence 809541,
9	19.2	66.2	610	6 US-09-925-065A-883719	Sequence 883719,
10	19	65.5	200	12 US-11-098-686-6941	Sequence 6941, Ap
11	19	65.5	596	6 US-09-925-065A-717454	Sequence 717454,
12	19	65.5	617	6 US-09-925-065A-575086	Sequence 575086,
13	19	65.5	622	6 US-09-925-065A-762355	Sequence 762355,
14	19	65.5	1926	12 US-11-098-686-9784	Sequence 9784, Ap
15	19	65.5	27733	8 US-11-829-826B-18	Sequence 18, Appli
16	19	65.5	1457619	12 US-11-098-686-8739	Sequence 8739, A
17	18.6	64.1	502	6 US-09-925-065A-551876	Sequence 551876,
18	18.6	64.1	556	6 US-09-925-065A-484856	Sequence 484856,
19	18.6	64.1	159138	8 US-10-995-561-13230	Sequence 13230, A
20	18.6	64.1	159781	12 US-11-121-086-92	Sequence 92, Appli

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RESULT 2
US-10-514-878A-4
; Sequence 4, Application US/10514878A
; Publication No. US2006035319A1
; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimeric Human Papillom
; TYPE OF INVENTION: Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent version 3.1
; SEQ ID NO 4
; LENGTH: 1518

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; TYPE: DNA  
; ORGANISM: Human papillomavirus  
US-10-514-878A-4  
  
Query Match 83.4%; Score 24.2; DB 7; Length 1518;  
Best Local Similarity 89.7%; Pred. No. 0.72;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GATGGTGATATGTTAGATACAGGATTGG 29  
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Db 589 GATGGTGATATGTTAGTACTGCTTTGG 617

RESULT 3  
US-10-514-878A-6  
; Sequence 6, Application US/10514878A  
; Publication No. US20060035319A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Cape Town  
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Methods of Preparing the Particles  
; FILE REFERENCE: 10/514,878  
; CURRENT APPLICATION NUMBER: US/10/514,878A  
; CURRENT FILING DATE: 2004-11-16  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 1518  
; TYPE: DNA  
; ORGANISM: Human papillomavirus  
US-10-514-878A-6  
  
Query Match 83.4%; Score 24.2; DB 7; Length 1518;  
Best Local Similarity 89.7%; Pred. No. 0.72;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GATGGTGATATGTTAGTACTGCTTTGG 29  
|||||  
Db 589 GATGGTGATATGTTAGTACTGCTTTGG 617

RESULT 4  
US-10-514-878A-8  
; Sequence 8, Application US/10514878A  
; Publication No. US20060035319A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Cape Town  
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Methods of Preparing the Particles  
; FILE REFERENCE: 10/514,878  
; CURRENT APPLICATION NUMBER: US/10/514,878A  
; CURRENT FILING DATE: 2004-11-16  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 1518  
; TYPE: DNA  
; ORGANISM: Human papillomavirus  
US-10-514-878A-8  
  
Query Match 83.4%; Score 24.2; DB 7; Length 1518;  
Best Local Similarity 89.7%; Pred. No. 0.72;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GATGGTGATATGTTAGTACTGCTTTGG 29  
|||||  
Db 589 GATGGTGATATGTTAGTACTGCTTTGG 617

RESULT 5  
US-10-514-878A-10  
; Sequence 10, Application US/10514878A  
; Publication No. US20060035319A1

; GENERAL INFORMATION:  
; APPLICANT: University of Cape Town  
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Methods of Preparing the Particles  
; FILE REFERENCE: 10/514,878  
; CURRENT APPLICATION NUMBER: US/10/514,878A  
; CURRENT FILING DATE: 2004-11-16  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 1518  
; TYPE: DNA  
; ORGANISM: Human papillomavirus  
US-10-514-878A-10  
  
Query Match 83.4%; Score 24.2; DB 7; Length 1518;  
Best Local Similarity 89.7%; Pred. No. 0.72;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GATGGTGATATGTTAGTACTGCTTTGG 29  
|||||  
Db 589 GATGGTGATATGTTAGTACTGCTTTGG 617

RESULT 6  
US-10-514-878A-12  
; Sequence 12, Application US/10514878A  
; Publication No. US20060035319A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Cape Town  
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Methods of Preparing the Particles  
; FILE REFERENCE: 10/514,878  
; CURRENT APPLICATION NUMBER: US/10/514,878A  
; CURRENT FILING DATE: 2004-11-16  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 1518  
; TYPE: DNA  
; ORGANISM: Human papillomavirus  
US-10-514-878A-12  
  
Query Match 83.4%; Score 24.2; DB 7; Length 1518;  
Best Local Similarity 89.7%; Pred. No. 0.72;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GATGGTGATATGTTAGTACTGCTTTGG 29  
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Db 589 GATGGTGATATGTTAGTACTGCTTTGG 617

RESULT 7  
US-11-179-478-1  
; Sequence 1, Application US/11179478  
; Publication No. US20050249745A1  
; GENERAL INFORMATION:  
; APPLICANT: BURGER, Alexander  
; APPLICANT: HALLEK, Michael  
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
; TITLE OF INVENTION: FORMULATIONS AND METHODS OF USE  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; FILING DATE: US/11/179,478  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA: US/10/654,129  
;; FILING DATE: 04-Sep-2003  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sandercock, Colin G.  
;; REGISTRATION NUMBER: 31,298  
;; REFERENCE/DOCKET NUMBER: 37067/102  
;; TELEPHONE: (202) 672-5300  
;; TELEFAX: (202) 672-5399  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1518 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..1515  
US-11-179-478-1

Query Match 83.4%; Score 24.2; DB 12; Length 1518;  
Best Local Similarity 89.7%; Pred. No. 0.72; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATGGTGATGCTAGATACAGGATTGG 29  
DB 589 GATGGTGATGCTAGATACAGGATTGG 617

RESULT 8  
US-09-925-065A-809541  
; Sequence 809541, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 809541  
; LENGTH: 623  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-809541

Query Match 67.6%; Score 19.6; DB 6; Length 623;  
Best Local Similarity 84.6%; Pred. No. 59;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GATGGTGATGCTAGATACAGGATT 26  
DB 564 GATGGTGCTGCTAGATACAGGATT 589

RESULT 9  
US-09-925-065A-883719  
; Sequence 883719, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 883719  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-883719

Query Match 66.2%; Score 19.2; DB 6; Length 610;  
Best Local Similarity 87.5%; Pred. No. 88;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGTGATGCTAGATACAGGATT 26  
DB 409 TGGTGATGCTAGATACAGGATT 432

RESULT 10  
US-11-098-686-6941/c  
; Sequence 6941, Application US/11098686  
; Publication No. US20060024696A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.  
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES  
; FILE REFERENCE: 09531-128001  
; CURRENT APPLICATION NUMBER: US/11/098,686  
; PRIOR FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US03/31318  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: US 60/416,395  
; PRIOR FILING DATE: 2002-10-04  
; NUMBER OF SEQ ID NOS: 11433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6941  
; LENGTH: 200  
; TYPE: DNA  
; ORGANISM: Lawsonia intracellularis  
US-11-098-686-6941

Query Match 65.5%; Score 19; DB 12; Length 200;  
Best Local Similarity 81.5%; Pred. No. 82;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 199 ATGGTGATGCTAGATACAGGATTG 173

RESULT 11

RESULT 15



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US-10-829-826B-18
; Sequence 18, Application US/10829826B
; Publication No. US20050266397A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Blyn, Lawrence B.
; APPLICANT: Hall, Thomas A.
; APPLICANT: Massire, Christian
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF CORONAVIRUSES
; FILE REFERENCE: IBIS0075-100 (IBIS-0058US)
; CURRENT APPLICATION NUMBER: US/10/829,826B
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 27733
; TYPE: DNA
; ORGANISM: Coronavirus
US-10-829-826B-18

Query Match      65.5%; Score 19; DB 8; Length 27733;
Best Local Similarity 81.5%; Pred. No. 2.8e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 TGGTGATATGCTAGATACAGGATTGG 29
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Db      26684 TGGTTATAGTAGTAGACAGGATTGG 26710

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Job time : 459 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:50:08 ; Search time 380.5 Seconds  
(without alignments)  
507.953 Million cell updates/sec

Title: US-10-720-424b-8

Perfect score: 29  
Sequence: 1 ggcgcagaggtaccatagagccactagg 29

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	24.2	83.4	1484	2	AAX89755
5	24.2	83.4	1494	3	AAD01237
6	24.2	83.4	1500	3	AAD01238
7	24.2	83.4	1517	2	AAQ47167
8	24.2	83.4	1517	2	AAQ47166
9	24.2	83.4	1517	2	AAV09856
10	24.2	83.4	1517	2	AAV09855
11	24.2	83.4	1517	2	AAV25818
12	24.2	83.4	1517	2	AAV25817
13	24.2	83.4	1517	2	AAV12161
14	24.2	83.4	1517	2	AAV12162
15	24.2	83.4	1517	2	AAV23923
16	24.2	83.4	1517	2	AAV24099
17	24.2	83.4	1517	2	AAX15111
18	24.2	83.4	1517	2	AAX15112
19	24.2	83.4	1517	3	AAX40564

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C 22	24.2	83.4	1517	10	ADC26169
C 23	24.2	83.4	1517	12	ADG62855
C 24	24.2	83.4	1517	12	ADG62854
C 25	24.2	83.4	1518	2	AAX37566
C 26	24.2	83.4	1518	3	AAX248174
C 27	24.2	83.4	1518	9	ABX11395
C 28	24.2	83.4	1518	9	ABX11396
C 29	24.2	83.4	1518	9	ADA27368
C 30	24.2	83.4	1518	9	ADA27369
C 31	24.2	83.4	1518	9	ADA92547
C 32	24.2	83.4	1518	9	ADA92546
C 33	24.2	83.4	1518	9	ADA14296
C 34	24.2	83.4	1518	9	ADA14295
C 35	24.2	83.4	1518	9	AAD58576
C 36	24.2	83.4	1518	9	AAD58577
C 37	24.2	83.4	1518	10	ACC47502
C 38	24.2	83.4	1518	10	ACC47504
C 39	24.2	83.4	1518	12	ADF83436
C 40	24.2	83.4	1518	12	ADF83440
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C 42	24.2	83.4	1518	12	ADF83434
C 43	24.2	83.4	1518	12	ADF83444
C 44	24.2	83.4	1518	12	ADF83442
C 45	24.2	83.4	1518	12	ADN49002

#### ALIGNMENTS

RESULT 1

ADQ27978

ID ADQ27978 standard; DNA; 29 BP.

XX AC ADQ27978;

XX DT 09-SEP-2004 (first entry)

XX DE Human papillomavirus genotype detection PCR primer #8.

XX KW ss; primer; detection; diagnosis; amplification;

XX KW Human papillomavirus genotype; cervical-neoplasia;

XX KW oncogenic high-risk group.

XX OS Human papillomavirus.

XX PN WO2004050917-A1.

XX PD 17-JUN-2004.

XX PF 28-NOV-2003; 2003WO-KR002608.

XX PR 29-NOV-2002; 2002KR-00075370.

XX PR 31-JUL-2003; 2003KR-00053147.

XX (ALBI-) ALBIOMED CO LTD.

XX PI Lee S, Kim Y, Yu K, Kim S, Cha K, Ko J;

XX DR WPI; 2004-450746/42.

XX PT New general primer or primer pair, useful for amplifying and detecting, or for use in a nucleic acid amplification process for amplifying Human Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV genotypes.

XX PS Claim 2; SEQ ID NO 8; 71pp; English.

XX CC The invention relates to a general primer or primer pair for amplifying and detecting or for use in a nucleic acid amplification process for amplifying Human Papillomavirus (HPV) genotypes. The general primers are useful for amplifying cervical-neoplasia related HPV genotypes including



KW assay; cancer; virus; HPV; ss.  
 XX Synthetic.  
 OS Human papillomavirus.  
 XX  
 XX  
 PN W09929890-A2.  
 XX  
 PD 17-JUN-1999.  
 XX  
 XX  
 PF 11-DEC-1998; 98WO-US026447.  
 XX  
 PR 12-DEC-1997; 97US-0069426P.  
 PR 05-JAN-1998; 98US-0070486P.  
 PR 17-APR-1998; 98US-0082167P.  
 XX  
 PA (DIGE-) DIGENE CORP.  
 XX  
 XX Lorincz AT;  
 XX  
 DR WPI; 1999-443850/37.  
 XX  
 PT New method for assessing Human Papilloma Virus (HPV) infection by  
 PT comparison of gene expression levels.  
 XX  
 PS Disclosure; Fig 4; 35pp; English.  
 XX  
 CC This nucleotide probe is specific for the HPV16 Human Papilloma Virus  
 CC (HPV) gene. The degree of HPV infection can be assessed, by measuring the  
 CC levels of expression of genes involved in the diseased state, and  
 CC comparing the expression to each other or to reference genes. (Updated on  
 CC 27-AUG-2003 to correct OS field.)  
 XX  
 XX Sequence 1484 BP; 481 A; 285 C; 277 G; 441 T; 0 U; 0 Other;  
 SQ  
 Query Match 83.4%; Score 24.2; DB 2; Length 1484;  
 Best Local Similarity 89.7%; Pred. No. 0.18; Mismatches 0; Gaps 0;  
 Matches 26; Conservative 0; Indels 3; Indels 0; Gaps 0;  
 OY 1 CGCTCAGAGGTTACCATAGAGCCACTAGG 29  
 DB 890 GCATCAGAGGTTAACCATAGAGCCACTAGG 862  
 RESULT 5  
 AAD01237/c  
 ID AAD01237 standard; DNA; 1494 BP.  
 XX  
 XX AAD01237;  
 AC AAD01237;  
 XX  
 DT 04-OCT-2000 (first entry)  
 XX  
 XX Chimeric biotin-binding human papillomavirus mutant L1 protein-168 DNA.  
 DE  
 DE Human papillomavirus; HPV; L1 protein; L2 protein; biotin; chimeric;  
 KW cytosolic; antiviral; gene therapy; vaccine; capsomere; VLP;  
 KW virus-like particle; viral antigen; tumour; cytotoxin; cytokine; IL;  
 KW interleukin; chemotherapeutic agent; radioactive agent; mutant; ds.  
 XX  
 XX Human papillomavirus type 16.  
 OS Unidentified.  
 OS Chimeric.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 1..1494  
 FT /tag= a  
 FT /product= "Chimeric protein 168 containing human  
 FT papillomavirus 16 mutant L1 protein fused to biotin-  
 FT binding peptide at the C-terminal"  
 FT 1450..1494  
 FT misc\_feature /tag= b  
 FT /note= "Biotin-binding peptide DNA"  
 FT  
 FT  
 XX W0200031128-A1.

XX 02-JUN-2000.  
 PD  
 XX  
 XX 22-NOV-1999; 99WO-US027555.  
 PF  
 XX  
 PR 23-NOV-1998; 98US-0109510P.  
 PR 06-OCT-1999; 99US-00413611.  
 XX  
 XX (LOYO ) UNIV LOYOLA CHICAGO.  
 PA  
 XX  
 XX Mueller M, Kast WM, Nieland JD, Velders MP;  
 PI  
 XX  
 XX WPI; 2000-400041/34.  
 DR P-PSDB; AAY71464.  
 XX  
 XX Chimeric protein comprising a papillomavirus L1 or L2 protein and a  
 PT biotin-binding polypeptide, useful for delivering substances such as  
 PT proteins, nucleic acids and lipids into cells, particularly  
 PT papillomavirus infected cells.  
 XX  
 XX Example 1; Page 15-18; 27pp; English.  
 PS  
 XX The patent discloses a chimeric protein comprising papillomavirus L1 or  
 CC L2 protein and a biotin-binding polypeptide. Capsomere, papillomavirus or  
 CC virus-like particle (VLP) comprising the chimeric protein is used for  
 CC delivering a wide variety of biotinylated compounds e.g. proteins,  
 CC nucleic acids and lipids into cells, particularly papillomavirus infected  
 CC cells. The chimeric protein may also be used as a vaccine when the  
 CC biotinylated substance is a viral antigen e.g. papillomavirus E2 or E7  
 CC proteins. It may be useful for treating tumours or other papillomavirus-  
 CC related lesions when the substance is a cytotoxin, chemotherapeutic  
 CC agent, radioactive agent, or a gene encoding a cytokine or interleukin.  
 CC The present sequence is a DNA encoding a chimeric protein 168 consisting  
 CC of human papillomavirus 16 (HPV-16) mutant L1 protein fused to a biotin-  
 CC binding peptide at the C-terminus. The L1 protein was derived from the  
 CC wild-type sequence by deleting the amino acid Cys428. The modification of  
 CC was done to prevent assembly of VLPs while allowing the production of  
 CC capsomeres at high efficiencies  
 XX  
 XX Sequence 1494 BP; 462 A; 292 G; 449 T; 0 U; 0 Other;  
 SQ  
 Query Match 83.4%; Score 24.2; DB 3; Length 1494;  
 Best Local Similarity 89.7%; Pred. No. 0.18; Mismatches 0; Gaps 0;  
 Matches 26; Conservative 0; Indels 3; Indels 0; Gaps 0;  
 OY 1 CGCTCAGAGGTTACCATAGAGCCACTAGG 29  
 DB 911 GCATCAGAGGTTACCATAGAGCCACTAGG 883  
 RESULT 6  
 AAD01238/c  
 ID AAD01238 standard; DNA; 1500 BP.  
 XX  
 XX AAD01238;  
 AC AAD01238;  
 XX  
 DT 04-OCT-2000 (first entry)  
 XX  
 XX Chimeric biotin-binding human papillomavirus mutant L1 protein-169 DNA.  
 DE  
 DE Human papillomavirus; HPV; L1 protein; L2 protein; biotin; chimeric;  
 KW cytosolic; antiviral; gene therapy; vaccine; capsomere; VLP;  
 KW virus-like particle; viral antigen; tumour; cytotoxin; cytokine; IL;  
 KW interleukin; chemotherapeutic agent; radioactive agent; mutant; ds.  
 XX  
 XX Human papillomavirus type 16.  
 OS Unidentified.  
 OS Chimeric.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 1..1500  
 FT /tag= a  
 FT /product= "Chimeric protein 169 containing human



PI Lowy DR, Schiller JT, Kirnbauer R;  
 XX WPI; 1993-249995/31.  
 DR P-PSDB; AAW38807.  
 XX  
 PT Recombinant papilloma virus capsid proteins - for vaccines against  
 PT papilloma virus and for diagnosis of virus infection.  
 XX  
 XX Example 1; Page 32-34; 45pp; English.  
 PS  
 CC The sequences given in AAQ47166-67 encode the L1 capsid proteins from  
 CC bovine and human papillomavirus respectively. These sequences may be  
 CC inserted into a baculovirus transfer vector and operatively expressed by  
 CC a promoter of the vector, and the capsid protein produced by transformed  
 CC cells. The capsid proteins may be used in vaccines to induce high-titre  
 CC neutralising antibody response in vertebrates. (Note: Revised entry  
 CC submitted to correct the patent number format of US Government-owned NTIS  
 CC applications to prevent clashes with ongoing US granted patent numbers.  
 CC For further information please visit the Derwent web site at  
 CC www.derwent.com/dwpi/updates/ntis\_us.html.) (Updated on 25-MAR-2003 to  
 CC correct PF field.)  
 XX  
 SQ Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;  
 Query Match 83.4%; Score 24.2; DB 2; Length 1517;  
 Best Local Similarity 89.7%; Pred. No. 0.18;  
 Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GCGTCAGAGGTACCATAGAGCCACTAGG 29  
 |||||  
 DB 911 GCATCAGAGGTAAACCTAGACCACTAGG 883  
 |||||  
 RESULT 9  
 AAV09856/c  
 ID AAV09856 standard; DNA; 1517 BP.  
 XX  
 AC AAV09856;  
 XX  
 DT 26-MAY-1998 (first entry)  
 XX  
 DE HPV16 recombinant L1 capsid protein DNA.  
 XX  
 KW Capsid protein; L1; HPV16; vaccine; prevention; treatment; self-assembly;  
 KW viral protein; capsomer; capsid; antigenic epitope; ss.  
 XX  
 OS Human papillomavirus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1517  
 FT /\*tag= a  
 FT /product= "L1"  
 FT /note= "partial recombinant capsid protein sequence"  
 XX  
 PN US5716620-A.  
 XX  
 PD 10-FEB-1998.  
 XX  
 PF 07-JUN-1995; 95US-00475783.  
 XX  
 PR 03-SEP-1992; 92US-00941371.  
 PR 16-MAR-1993; 93US-00032869.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Kirnbauer R, Lowy DR, Schiller JT;  
 XX  
 DR WPI; 1998-158363/14.  
 DR P-PSDB; AAW39904.  
 XX  
 PT Vaccine against human papilloma virus - comprises HPV16 L1 polypeptide.  
 PS Claim 2; Col 21-24; 20pp; English.

XX This sequence encodes a recombinant L1 capsid protein from Human  
 CC Papillomavirus strain 16 (HPV16). This recombinant form of viral protein  
 CC is capable of self-assembly into capsomer structures and viral capsids  
 CC that comprise conformational antigenic epitopes can be used as a vaccine  
 CC for the prevention or treatment of papillomavirus infections in  
 CC vertebrates. The vaccine comprises a unit dose of a composition  
 CC containing a self assembled HPV16 with at least 1 papillomavirus L1  
 CC conformational epitope  
 XX  
 SQ Sequence 1517 BP; 487 A; 291 C; 286 G; 453 T; 0 U; 0 Other;  
 Query Match 83.4%; Score 24.2; DB 2; Length 1517;  
 Best Local Similarity 89.7%; Pred. No. 0.18;  
 Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GCGTCAGAGGTACCATAGAGCCACTAGG 29  
 |||||  
 DB 911 GCATCAGAGGTAAACCTAGACCACTAGG 883  
 |||||  
 RESULT 10  
 AAV09855/c  
 ID AAV09855 standard; DNA; 1517 BP.  
 XX  
 AC AAV09855;  
 XX  
 DT 26-MAY-1998 (first entry)  
 XX  
 DE HPV16 L1 capsid protein DNA.  
 XX  
 KW Capsid protein; L1; HPV16; vaccine; prevention; treatment; self-assembly;  
 KW viral protein; capsomer; capsid; antigenic epitope; ss.  
 XX  
 OS Human papillomavirus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1517  
 FT /\*tag= a  
 FT /product= "L1"  
 FT /note= "partial capsid protein sequence"  
 XX  
 PN US5716620-A.  
 XX  
 PD 10-FEB-1998.  
 XX  
 PF 07-JUN-1995; 95US-00475783.  
 XX  
 PR 03-SEP-1992; 92US-00941371.  
 PR 16-MAR-1993; 93US-00032869.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Kirnbauer R, Lowy DR, Schiller JT;  
 XX  
 DR WPI; 1998-158363/14.  
 DR P-PSDB; AAW39903.  
 XX  
 PT Vaccine against human papilloma virus - comprises HPV16 L1 polypeptide.  
 PS Disclosure; Col 17-20; 20pp; English.  
 XX  
 CC This sequence encodes the L1 capsid protein from Human Papillomavirus  
 CC strain 16 (HPV16). A recombinant form of this viral protein which is  
 CC capable of self-assembly into capsomer structures and viral capsids that  
 CC comprise conformational antigenic epitopes can be used as a vaccine for  
 CC the prevention or treatment of papillomavirus infections in vertebrates.  
 CC The vaccine comprises a unit dose of a composition containing a self  
 CC assembled HPV16 with at least 1 papillomavirus L1 conformational epitope  
 XX  
 SQ Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;  
 Query Match 83.4%; Score 24.2; DB 2; Length 1517;

Best Local Similarity 89.7%; Pred. No. 0.18; Mismatches 0; Indels 3; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29  
 |||||  
 Db 911 GCATCAGAGGTAACCATAGAGCCACTAGG 883

## RESULT 11

AAV25818/c  
 ID AAV25818 standard; DNA; 1517 BP.

XX AAV25818;

XX 10-JUL-1998 (first entry)

XX Human papillomavirus proto-type HPV 16 L1 genome 5637-7155.

XX Human papillomavirus; HPV 16; L1 gene; immunisation; capsid;  
 conformational epitope; vaccine; sequelae; vertebrate; ss.

XX Human papillomavirus.

XX Key Location/Qualifiers  
 CDS 1..1517

FT /\*tag= a  
 FT /product= "HPV 16 L1 proto-type"  
 FT /note= "no stop codon given"

XX US5744142-A.

XX 28-APR-1998.

XX 07-JUN-1995; 95US-00475782.

XX 03-SEP-1992; 92US-00941371.

XX 16-MAR-1993; 93US-00032869.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Schiller JT, Kirnbauer R, Lowy DR;

XX WPI; 1998-271010/24.

XX P-PSDB; AAW53486.

PT Immunisation of mammals and humans against papillomavirus infection -  
 PT comprises administering recombinant self-assembled capsid proteins  
 PT containing conformational epitopes.

XX Disclosure; Col 17-20; 20pp; English.

XX The present sequence represents the human papillomavirus proto-type HPV  
 CC 16 L1 genome 5637-7155, from the present invention. The present invention  
 CC describes the immunisation of a host mammal against a papillomavirus  
 CC comprising administering to the host, according to an immunising  
 CC schedule, a self-assembled Human Papilloma Virus (HPV16) capsid (I)  
 CC containing at least 1 papillomavirus L1 conformational epitope. The  
 CC papillomavirus L1 conformational epitopes are produced by letting a  
 CC genetic construct comprising a papillomavirus L1 gene direct recombinant  
 CC expression of the conformational epitope in a transformed eukaryotic host  
 CC cell by self-assembly of papillomavirus capsids containing a L1  
 CC polypeptide having an amino acid sequence encoded by the nucleic acid  
 CC sequence given in the specification (see AAV25817). (I) are useful for  
 CC the diagnosis of and as vaccines for the prevention of papillomavirus  
 CC infections and their benign and malignant sequelae in vertebrates.

XX Recombinant conformed papillomavirus proteins are provided which can be  
 CC used to produce renewable papillomavirus reagents of any selected species  
 CC and type in cell culture. The self-assembled recombinant L1 capsid  
 CC protein has the efficacy of intact papillomavirus particles to induce  
 CC high levels of neutralising antiserum, in contrast to prior art L1  
 CC protein extracted from recombinant bacteria or denatured virions

XX Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;

Query Match 83.4%; Score 24.2; DB 2; Length 1517;  
 Best Local Similarity 89.7%; Pred. No. 0.18;  
 Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29  
 |||||  
 Db 911 GCATCAGAGGTAACCATAGAGCCACTAGG 883

## RESULT 12

AAV25817/c

ID AAV25817 standard; DNA; 1517 BP.

XX AAV25817;

XX 10-JUL-1998 (first entry)

XX Human papillomavirus wild-type HPV 16 L1 conformational epitope gene.

XX Human papillomavirus; HPV 16; L1 gene; immunisation; capsid;  
 conformational epitope; vaccine; sequelae; vertebrate; ss.

XX Human papillomavirus.

XX Key Location/Qualifiers  
 CDS 1..1517

FT /\*tag= a  
 FT /product= "HPV 16 L1 conformational epitope"  
 FT /note= "no stop codon given"

XX US5744142-A.

XX 28-APR-1998.

XX 07-JUN-1995; 95US-00475782.

XX 03-SEP-1992; 92US-00941371.

XX 16-MAR-1993; 93US-00032869.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Schiller JT, Kirnbauer R, Lowy DR;

XX WPI; 1998-271010/24.

XX P-PSDB; AAW53486.

PT Immunisation of mammals and humans against papillomavirus infection -  
 PT comprises administering recombinant self-assembled capsid proteins  
 PT containing conformational epitopes.

XX Claim 1; Col 21-24; 20pp; English.

XX The present sequence encodes the human papillomavirus HPV 16 L1  
 CC conformational epitope, from the present invention. The present invention  
 CC describes the immunisation of a host mammal against a papillomavirus  
 CC comprising administering to the host, according to an immunising  
 CC schedule, a self-assembled Human Papilloma Virus (HPV16) capsid (I)  
 CC containing at least 1 papillomavirus L1 conformational epitope. The  
 CC papillomavirus L1 conformational epitopes are produced by letting a  
 CC genetic construct comprising a papillomavirus L1 gene direct recombinant  
 CC expression of the conformational epitope in a transformed eukaryotic host  
 CC cell by self-assembly of papillomavirus capsids containing a L1  
 CC polypeptide having an amino acid sequence encoded by the nucleic acid  
 CC sequence given in the specification (present sequence). (I) are useful  
 CC for the diagnosis of and as vaccines for the prevention of papillomavirus  
 CC infections and their benign and malignant sequelae in vertebrates.  
 CC Recombinant conformed papillomavirus proteins are provided which can be  
 CC used to produce renewable papillomavirus reagents of any selected species  
 CC and type in cell culture. The self-assembled recombinant L1 capsid  
 CC protein has the efficacy of intact papillomavirus particles to induce  
 CC high levels of neutralising antiserum, in contrast to prior art L1  
 CC protein extracted from recombinant bacteria or denatured virions



```
XX SQ Sequence 1517 BP; 487 A; 291 C; 286 G; 453 T; 0 U; 0 Other;
Query Match 83.4%; Score 24.2; DB 2; Length 1517;
Best Local Similarity 89.7%; Pred. No. 0.18;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
||| ||||| ||||| ||||| ||||| |||||
Db 911 GCATCAGAGGTTAACCATAGAACCACTAGG 883

RESULT 13
AAV12161/c
ID AAV12161 standard; DNA; 1517 BP.
XX AC AAV12161;
XX DT 05-MAY-1998 (first entry)
XX DE Human papillomavirus wild-type L1 gene.
XX KW Human; papillomavirus; bovine; L1 conformational protein; antibody;
XX KW detection; diagnosis; ss.
XX OS Human papillomavirus.
XX FH Key Location/Qualifiers
XX CDS 1..1517
XX FT /*tag= a
XX FT /product= "L1"
XX FT /note= "no stop codon given"
XX PN US5709996-A.
XX PD 20-JAN-1998.
XX PF 07-JUN-1995; 95US-00472673.
XX PR 03-SEP-1992; 92US-00941371.
XX PR 16-MAR-1993; 93US-00032869.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Schiller JT, Kirnbauer R, Lowy DR;
XX DR WPI; 1998-109811/10.
XX DR P-PSDB; AAW44142.
XX PT Assay for papilloma virus - using antibody directed against recombinant
XX L1 polypeptide.
XX PS Claim 1; Col 21-24; 34pp; English.
XX CC An method has been developed for detecting papilloma virus in a specimen
XX from a mammal. The method comprises contacting the sample with an
XX antibody and detecting any antibody binding. The antibody is a polyclonal
XX or monoclonal antibody produced by transforming a eukaryotic host cell
XX with a genetic construct containing a papillomavirus L1 gene so that the
XX cell expresses self-assembled papillomavirus-like particles containing at
XX least 1 papillomavirus L1 conformational epitope. The present sequence
XX encodes wild-type human papillomavirus L1 polypeptide. The method is for
XX the diagnosis of papillomavirus infections in mammals
XX SQ Sequence 1517 BP; 487 A; 291 C; 286 G; 453 T; 0 U; 0 Other;
Query Match 83.4%; Score 24.2; DB 2; Length 1517;
Best Local Similarity 89.7%; Pred. No. 0.18;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
||| ||||| ||||| ||||| ||||| |||||
Db 911 GCATCAGAGGTTAACCATAGAACCACTAGG 883

RESULT 14
AAV12162/c
ID AAV12162 standard; DNA; 1517 BP.
XX AC AAV12162;
XX DT 05-MAY-1998 (first entry)
XX DE Human papillomavirus prototype L1 gene.
XX KW Human; papillomavirus; bovine; L1 conformational protein; antibody;
XX KW detection; diagnosis; ss.
XX OS Human papillomavirus.
XX FH Key Location/Qualifiers
XX CDS 1..1517
XX FT /*tag= a
XX FT /product= "L1"
XX FT /note= "no stop codon given"
XX PN US5709996-A.
XX PD 20-JAN-1998.
XX PF 07-JUN-1995; 95US-00472673.
XX PR 03-SEP-1992; 92US-00941371.
XX PR 16-MAR-1993; 93US-00032869.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Schiller JT, Kirnbauer R, Lowy DR;
XX DR WPI; 1998-109811/10.
XX DR P-PSDB; AAW44143.
XX PT Assay for papilloma virus - using antibody directed against recombinant
XX L1 polypeptide.
XX PS Disclosure; Col 17-20; 34pp; English.
XX CC An method has been developed for detecting papilloma virus in a specimen
XX from a mammal. The method comprises contacting the sample with an
XX antibody and detecting any antibody binding. The antibody is a polyclonal
XX or monoclonal antibody produced by transforming a eukaryotic host cell
XX with a genetic construct containing a papillomavirus L1 gene so that the
XX cell expresses self-assembled papillomavirus-like particles containing at
XX least 1 papillomavirus L1 conformational epitope. The present sequence
XX encodes prototype human papillomavirus L1 polypeptide. The method is for
XX the diagnosis of papillomavirus infections in mammals
XX SQ Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;
Query Match 83.4%; Score 24.2; DB 2; Length 1517;
Best Local Similarity 89.7%; Pred. No. 0.18;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
||| ||||| ||||| ||||| ||||| |||||
Db 911 GCATCAGAGGTTAACCATAGAACCACTAGG 883

RESULT 15
AAV23923/c
ID AAV23923 standard; DNA; 1517 BP.
XX AC AAV23923;
XX DT 17-OCT-2003 (revised)
XX DT 10-AUG-1998 (first entry)
```

XX HPV16 L1 gene #1.  
DE  
XX Human papillomavirus 16; HPV17; L1 gene; infection; antibody detection;  
KW ss.  
XX Human papillomavirus type 16.  
OS  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1515  
FT /\*tag= a  
FT /note= "no stop codon given"  
XX  
XX US5756284-A.  
XX  
XX 26-MAY-1998.  
XX  
XX 07-JUN-1995; 95US-00472672.  
XX  
XX 03-SEP-1992; 92US-00941371.  
PR 16-MAR-1993; 93US-00032869.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Kirnbauer R, Lowy DR, Schiller JT;  
PI  
XX WPI; 1998-321522/28.  
DR P-PSDB; AAW54034.  
XX  
XX Assay for antibodies to papilloma virus - using self-assembled  
PT papillomavirus-like particles comprising L1 polypeptide.  
XX  
XX Disclosure; Col 17-20; 21pp; English.  
XX  
XX This sequence encodes the human papillomavirus 16 (HPV16) L1 gene  
CC protein. The protein can be used in the method of the invention for  
CC detecting antibodies to a papilloma virus in a sample from a mammal. The  
CC method comprises: (a) providing self-assembled papillomavirus-like  
CC particles comprising a L1 polypeptide, where the self-assembled  
CC papillomavirus-like particles comprise at least one L1 conformational  
CC epitope and are produced by permitting a genetic construct comprising a  
CC papillomavirus L1 gene to direct recombinant expression in a transformed  
CC eukaryotic host cell; (b) contacting the sample with the self-assembled  
CC papillomavirus-like particles; and (c) detecting any antibody binding to  
CC the self-assembled papillomavirus-like particles. The method can be used  
CC for detecting antibodies to HPV16 as an indication of infection. (Updated  
CC on 17-OCT-2003 to standardise OS field)  
XX  
XX Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;  
SQ

Query Match 83.4%; Score 24.2; DB 2; Length 1517;  
Best Local Similarity 89.7%; Pred. No. 0.18;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTACCATAGCCACTAGG 29  
||| ||||| ||||| ||||| |||||  
Db 911 GCATCAGAGGTAACCATAGCCACTAGG 883.

Search completed: March 5, 2006, 22:12:08  
Job time : 381.5 secs

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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:59:29 ; Search time 3168 Seconds  
(without alignments)  
428.291 Million cell updates/sec

Title: US-10-720-424b-8  
Perfect score: 29  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues  
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	69.0	589	DN408692	DN408692 LIB4007-0
2	20	69.0	798	BX227374	BX227374 Danio rer
3	20	69.0	828	BX216514	BX216514 Danio rer
4	19.8	68.3	191	AJ760626	AJ760626 AJ760626
5	19.8	68.3	280	AJ763893	AJ763893 AJ763893
6	19.6	67.6	486	AZ221755	AZ221755 RPCI-23-5
7	19.6	67.6	537	AU243490	AU243490 AU243490
8	19.6	67.6	552	AZ256958	AZ256958 RPCI-23-1
9	19.6	67.6	601	DE105340	DE105340 Oryzias l
10	19.6	67.6	613	CV504457	CV504457 71003.1 M
11	19.6	67.6	765	CK260235	CK260235 EST706313
12	19.6	67.6	790	CK260232	CK260232 EST706310
13	19.6	67.6	803	DE114072	DE114072 Oryzias l
14	19.6	67.6	838	CR099508	CR099508 Forward s
15	19.6	67.6	990	CU110457	CU110457 ISB1-53J1
16	19.4	66.9	425	BZ161634	BZ161634 CH230-388
17	19.4	66.9	476	AQ93275	AQ93275 RPCI-23-3
18	19.4	66.9	503	BM529734	BM529734 fx44d08.Y
19	19.4	66.9	503	BM530649	BM530649 fx47c05.Y
20	19.4	66.9	591	CA875703	CA875703 K0943A01-
21	19.4	66.9	670	AJ730032	AJ730032 AJ730032
22	19.4	66.9	689	AZ501268	AZ501268 LM0340K04

C 23	19.4	66.9	1027	2	BG745404	BG745404 602723750
C 24	19.4	66.9	1307	3	BI457107	BI457107 603185348
C 25	19.2	66.2	496	1	AW321749	AW321749 uc38c03.Y
C 26	19.2	66.2	639	10	CZ735950	CZ735950 OC_Ba007
C 27	19.2	66.2	692	10	CZ815849	CZ815849 OC_Ba019
C 28	19.2	66.2	742	6	CF347434	CF347434 AGENCOURT
C 29	19.2	66.2	752	10	CZ864166	CZ864166 OC_Ba025
C 30	19.2	66.2	795	10	CZ783180	CZ783180 OC_Ba014
C 31	19.2	66.2	899	10	CG768184	CG768184 TCB48.4 B
C 32	19.2	66.2	2122	4	AK031646	AK031646 Mus muscu
C 33	19	65.5	361	9	B87751	B87751 RPCI11-30F1
C 34	19	65.5	744	10	BX208090	BX208090 Danio rer
C 35	19	65.5	763	9	CC903234	CC903234 t006115Ba
C 36	19	65.5	771	3	BQ158020	BQ158020 NF015B02P
C 37	19	65.5	775	5	BW938474	BW938474 BW938474
C 38	19	65.5	835	10	BX213865	BX213865 Danio rer
C 39	19	65.5	864	7	CK290626	CK290626 EST753340
C 40	19	65.5	902	7	CR575491	CR575491 CR575491
C 41	19	65.5	908	8	CA469660	CA469660 JGI_XZG39
C 42	19	65.5	908	10	CZ507804	CZ507804 GMW2-60H1
C 43	19	65.5	919	10	CZ505564	CZ505564 GMW2-11A1
C 44	19	65.5	925	10	CZ500920	CZ500920 GMW2-10G2
C 45	19	65.5	1062	6	CA495435	CA495435 AGENCOURT

## ALIGNMENTS

RESULT 1  
DN408692  
LOCUS DN408692 589 bp mRNA linear EST 07-MAR-2005  
DEFINITION LIB4007-010-Q6-K1-B3 LIB4007 Canis familiaris cDNA clone  
CLN9364981, mRNA sequence.  
ACCESSION DN408692.1 GI:60589913  
VERSION DN408692  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis  
REFERENCE 1 (bases 1 to 589)  
AUTHORS Staton,N.R.  
TITLE Direct Submission (Staton,N.R.)  
JOURNAL Unpublished (2005)  
COMMENT Contact: Nick Staton  
Tel: 636 247 6855  
Email: nicholas.r.staton@pfizer.com.  
FEATURES  
Location/Qualifiers  
source 1..589  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/strain="beagle"  
/db\_xref="taxon:9615"  
/clone="CLN9364981"  
/tissue\_type="Mesenteric Lymphnode"  
/lab\_host="DH10B"  
/clone\_lib="LIB4007"  
/note="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; k9  
mesenteric lymphnode"

Query Match 69.0%; Score 20; DB 8; Length 589;  
Best Local Similarity 82.1%; Pred. No. 2.6e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 CGGTCCAGGTTACCATAGCCACTAG 28  
|||||  
Db 111 GGGTCTTATCTTACCATAGCCACTAG 138  
|||||

RESULT 2  
BX227374

LOCUS BX227374 798 bp DNA linear GSS 29-JAN-2003  
 DEFINITION Danio rerio genomic clone DKEX-277E24, genomic survey sequence.  
 ACCESSION BX227374

VERSION BX227374.1 GI:28061524  
 KEYWORDS GSS.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 798)

AUTHORS Humphray,S.J., Huckle,E. and Durham,J.L.

TITLE Direct Submission  
 JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome  
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humphray@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the SP6 end of BAC 277E24. 277E24  
 is part of the Daniokey BAC Library created by R. Plasterk and N.V.  
 Keygene. Further details:  
 http://www.sanger.ac.uk/Projects/D\_rerio/.

FEATURES  
 Location/Qualifiers

1..798  
 /organism="Danio rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="DKEX-277E24"  
 /tissue\_type="Testis"  
 /notes="vector pindigobAC-536"

## ORIGIN

Query Match 69.0%; Score 20; DB 10; Length 798;

Best Local Similarity 82.1%; Pred. No. 2.8e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCGTCAGAGTTTACCATAGAGCCACTAG 28  
 |||||  
 DB 496 GCGTCAGTGTCTTACCATAGAGCCACG 523  
 |||||

## RESULT 3

BX216514

LOCUS BX216514 828 bp DNA linear GSS 13-MAR-2003  
 DEFINITION Danio rerio genomic clone DKEX-247D6, genomic survey sequence.  
 ACCESSION BX216514

VERSION BX216514.1 GI:28048400  
 KEYWORDS GSS.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 828)

AUTHORS Humphray,S.J., Huckle,E. and Durham,J.L.

TITLE Direct Submission  
 JOURNAL Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome  
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humphray@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the T7 end of BAC 247D6. 247D6 is  
 part of the Daniokey BAC Library created by R. Plasterk and N.V.  
 Keygene. Further details:  
 http://www.sanger.ac.uk/Projects/D\_rerio/.

FEATURES  
 Location/Qualifiers

1..828  
 /organism="Danio rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="DKEX-247D6"  
 /tissue\_type="Testis"  
 /notes="vector pindigobAC-536"

## ORIGIN

Query Match 69.0%; Score 20; DB 10; Length 828;

Best Local Similarity 82.1%; Pred. No. 2.8e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCGTCAGAGTTTACCATAGAGCCACTAG 28  
 |||||  
 DB 568 GCGTCAGTGTCTTACCATAGAGCCACG 595  
 |||||

## RESULT 4

AJ760626

LOCUS AJ760626 191 bp mRNA linear EST 03-JUN-2005  
 DEFINITION G0000500010E12F1, mRNA sequence.  
 ACCESSION AJ760626

VERSION AJ760626.1 GI:62941681

KEYWORDS EST.

SOURCE Gerbera hybrid cv. 'Terra Regina'

ORGANISM Gerbera hybrid cv. 'Terra Regina'

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; campanulids; Asterales; Asteraceae; Mutisioideae;  
 Mutisiae; Gerbera.  
 1 (bases 1 to 191)

AUTHORS Laitinen,R.A., Immanen,J., Auvinen,P., Rudd,S., Alatalo,E.R.,  
 Paulin,L., Ainasoja,M., Kotilainen,M., Koskela,S., Teeri,T.H. and  
 Elomaa,P.

TITLE Analysis of the floral transcriptome uncovers new regulators of  
 organ determination and gene families related to flower organ  
 differentiation in Gerbera hybrida (Asteraceae)  
 JOURNAL Genome Res. 15 (4), 475-486 (2005)  
 PUBMED 15781570

COMMENT Contact: Alatalo ER

Institute of Biotechnology

Vilkkinkaari 9, P.O. Box 56, 00014 University of Helsinki, FINLAND.

FEATURES  
 Location/Qualifiers

1..191  
 /organism="Gerbera hybrid cv. 'Terra Regina'"  
 /mol\_type="mRNA"  
 /cultivar="Terra Regina"  
 /db\_xref="taxon:226891"  
 /clone="G0000500010E12F1"  
 /tissue\_type="leaf, transgenic line 35S-gaga2"  
 /clone\_lib="G00005"

## ORIGIN

Query Match 68.3%; Score 19.8; DB 1; Length 191;

Best Local Similarity 91.3%; Pred. No. 2.6e+02;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCAGAGGTTTACCATAGAGCCACT 26  
 |||||

DB 32 TCAGAGGTTGCCATAGAGCCTCT 54  
 |||||

## RESULT 5

AJ763893

LOCUS AJ763893 280 bp mRNA linear EST 03-JUN-2005  
 DEFINITION G0000700010E06F1, mRNA sequence.  
 ACCESSION AJ763893

VERSION AJ763893.1 GI:58327558

KEYWORDS EST.

SOURCE Gerbera hybrid cv. 'Terra Regina'

ORGANISM Gerbera hybrid cv. 'Terra Regina'

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; campanulids; Asterales; Asteraceae; Mutisioideae;  
 Mutisiae; Gerbera.  
 1 (bases 1 to 280)

AUTHORS Laitinen,R.A., Immanen,J., Auvinen,P., Rudd,S., Alatalo,E.R.,  
 Paulin,L., Ainasoja,M., Kotilainen,M., Koskela,S., Teeri,T.H. and  
 Elomaa,P.

TITLE Analysis of the floral transcriptome uncovers new regulators of  
 organ determination and gene families related to flower organ

differentiation in Gerbera hybrida (Asteraceae)  
Genome Res. 15 (4), 475-486 (2005)

JOURNAL  
PURNED

COMMENT

Institute of Biotechnology  
Viikinkaari 9, P.O. Box 56, 00014 University of Helsinki, FINLAND.  
Location/Qualifiers

FEATURES  
source

1. .280  
/organism="Gerbera hybrid cv. 'Terra Regina'"  
/mol\_type="mRNA"  
/cultivar="Terra Regina"  
/db\_xref="taxon:226891"  
/clone="G0000700010E06F1"  
/tissue\_type="early petal"  
/dev\_stage="1-4"  
/clone\_lib="G00007"

ORIGIN

Query Match 68.3%; Score 19.8; DB 1; Length 280;  
Best Local Similarity 91.3%; Pred. No. 2.8e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCAGAGGTTTACCATAGAGCCACT 26  
Db 45 TCAGAGGTTGCCATAGAGCCTCT 67

RESULT 6

AZ221755  
LOCUS  
DEFINITION  
RPCI-23-50C11.TJ RPCI-23 Mus musculus genomic clone RPCI-23-50C11,  
genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS  
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,  
Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de  
Jong,P. and Fraser,C.M.  
Mouse BAC End Sequences from Library RPCI-23

TITLE

JOURNAL

COMMENT

Other GSSs: RPCI-23-50C11.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208

Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-23. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)  
or from Resea ch Genetics ([info@resgen.com](mailto:info@resgen.com)). BAC end page:  
[http://www.tigr.org/tdb/bac/ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html)  
Plate: 50 row: C column: 11  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
source

Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-23-50C11"  
/sex="Female"  
/lab\_host="DH10B"  
/clone\_lib="RPCI-23"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site\_1:  
EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or  
brain genomic DNA was isolated and partially digested  
with a combination of EcoRI and EcoRI Methyase. Size  
selected DNA was cloned into the pBACe3.6 vector at the  
EcoRI sites. The ligation products were transformed into  
DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 67.6%; Score 19.6; DB 9; Length 486;  
Best Local Similarity 84.6%; Pred. No. 3.9e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTTACCATAGAGCCACT 26  
Db 140 GCTTTAGAGATTACCACAGAGCCACT 165

RESULT 7

AU243490/c  
LOCUS  
DEFINITION  
AU243490 Medaka eye cDNA library (SNK01) Oryzias latipes cDNA clone  
NGX33.03h, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

ORGANISM

Oryzias latipes (Japanese medaka)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

REFERENCE

AUTHORS  
Sanaka,E., Hori,H., Naruse,K., Mitani,H. and Tanaka,M.  
Medaka EST analysis  
Unpublished (2001)  
Contact: Emi Sanaka

TITLE

JOURNAL

COMMENT

Department of Biological Sciences  
Graduate School of Science, Nagoya University  
Furo-cho, Chikusa-ku, Nagoya 464-8602, Japan  
Tel: 81-52-789-2973  
Fax: 81-52-789-2974  
Email: sanaka@bio.nagoya-u.ac.jp  
This clone was isolated from Medaka eye cDNA library (SNK01) 5'end.

FEATURES

source

1. 537  
Location/Qualifiers  
/organism="Oryzias latipes"  
/mol\_type="mRNA"  
/strain="wild type"  
/db\_xref="taxon:8090"  
/clone="NGY33.03h"  
/tissue\_type="eye"  
/dev\_stage="adult"  
/clone\_lib="Medaka eye cDNA library (SNK01)"  
/note="Wild samples from Okayama Pref. (Southern part of  
Japan)"

ORIGIN

Query Match 67.6%; Score 19.6; DB 1; Length 537;  
Best Local Similarity 84.6%; Pred. No. 4e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTTACCATAGAGCCACT 26  
Db 126 GAGTCAGGTTTCCATAGAGACACT 101

RESULT 8

AZ256958  
LOCUS  
DEFINITION  
RPCI-23-14903.TJ RPCI-23 Mus musculus genomic clone RPCI-23-14903,  
genomic survey sequence.

ACCESSION

AZ256958

```

VERSION      AZ256958.1  GI:9461222
KEYWORDS
SOURCE       Mus musculus (house mouse)
ORGANISM
REFERENCE    1 (bases 1 to 552)
AUTHORS      Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
              Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de
              Jong, P. and Fraser, C.M.
              Mouse BAC End Sequences from Library RPCI-23
              Unpublished (1999)
              Other_GSSs: RPCI-23-14903.TV
              Contact: Shaying Zhao
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 0200
              Fax: 301 838 0208
              Email: szhao@tigr.org
              Clones are derived from the mouse BAC library RPCI-23. For BAC
              library availability, please contact Pieter de Jong
              (pieter@dejong.med.buffalo.edu). Clones may be purchased from
              BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
              or from Resea ch Genetics (info@resgen.com). BAC end page:
              http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
              Plate: 149 row: 0 column: 3
              Seq primer: SP6
              Class: BAC ends.
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             /clone="RPCI-23-14903"
             /sex="female"
             /lab_host="DH10B"
             /clone_lib="RPCI-23"
             /notes="Organ: kidney/Brain; Vector: pBACE3.6; Site 1:
             EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
             brain genomic DNA was isolated and partially digested
             with a combination of EcoRI and EcoRI Methyase. Size
             selected DNA was cloned into the pBACE3.6 vector at the
             EcoRI sites. The ligation products were transformed into
             DH10B electrocompetent cells (BRL Life Technologies)."
ORIGIN
Query Match      67.6%; Score 19.6; DB 9; Length 552;
Best Local Similarity 84.6%; Pred. No. 4e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GCGTCAGAGTTACCATAGAGCCACT 26
DB      187  GCTTTAGAGATTACCACAGCCACT 212

RESULT 9
DE105340
LOCUS      DE105340
DEFINITION  Oryzias latipes DNA, forward end of BAC clone: Md0145B09, genomic
             survey sequence.
ACCESSION  DE105340
VERSION    DE105340.1  GI:71637508
KEYWORDS   GSS.
SOURCE     Oryzias latipes (Japanese medaka)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
             Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
             Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE  1

```

```

AUTHORS      Shimizu, N., Asakawa, S., Shimizu, A. and Sasaki, T.
TITLE       The BAC end sequence of Oryzias latipes
JOURNAL     Published Only in Database (2005)
REFERENCE   2 (bases 1 to 601)
AUTHORS      Shimizu, N., Asakawa, S., Sasaki, T. and Shimizu, A.
TITLE       Direct Submission
JOURNAL     Submitted (30-JUN-2005) Nobuyoshi Shimizu, Keio University, School
              of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku,
              Tokyo, 160-8582, Japan (E-mail: nshimizu@med.keio.ac.jp,
              Tel: 81-3-3351-2370, Fax: 81-3-3351-2370)
              Location/Qualifiers
              1..601
              /organism="Oryzias latipes"
              /mol_type="genomic DNA"
              /db_xref="taxon:8090"
              /clone="Md0145B09"
              /clone_lib="Medaka HDR BAC library"
              /note="This sequence is forward end of BAC clone
              Md0145B09."
ORIGIN
Query Match      67.6%; Score 19.6; DB 11; Length 601;
Best Local Similarity 84.6%; Pred. No. 4.1e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GCGTCAGAGTTACCATAGAGCCACT 26
DB      177  GAGTCAGTGGTTTCATAGAGACT 202

RESULT 10
CV504457/c
LOCUS      CV504457/c
DEFINITION  71003.1 Mixed Floral Solanum tuberosum cDNA clone 71003 5', mRNA
             sequence.
ACCESSION  CV504457
VERSION    CV504457.1  GI:53786814
KEYWORDS   EST..
SOURCE     Solanum tuberosum (potato)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
             asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE   1 (bases 1 to 613)
AUTHORS      Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De
              Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S.
              Generation of ESTs from a normalized developing floral bud library
              Unpublished (2004)
              Contact: Barry Flinn
              The Canadian Potato Genome Project - BioAtlantech
              921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
              Email: bflinn@bioatlantech.nb.ca
              Seq primer: T3.
FEATURES     Location/Qualifiers
             1..613
             /organism="Solanum tuberosum"
             /mol_type="mRNA"
             /cultivar="Shepody"
             /db_xref="taxon:4113"
             /clone="71003"
             /tissue_type="Floral buds"
             /lab_host="Xl10-Gold"
             /clone_lib="Mixed Floral"
             /note="Vector: pBluescript II SK(+); Site 1: EcoRI;
             Site 2: XhoI; supplier: Developmental series. Plants from
             pathogen-free Solanum tuberosum var. Shepody, clone 1756,
             nuclear stock were grown in a greenhouse under natural
             conditions. Developing floral buds were harvested at
             various sizes up to opening and pooled. RNA was isolated
             and used for library construction. A normalized library
             was constructed following a modified protocol of Bonaldo
             et al. (1996. Genome Research 6: 791-806)."
ORIGIN

```

```

Query Match      67.6%; Score 19.6; DB 7; Length 613;
Best Local Similarity 84.6%; Pred. No. 4.1e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3  GTCAGAGGTTACCATAGGCCACTAG 28
          |||||
          669  GTCAGAGGTTGCTTTTGAGCCACTAG 694

Db

RESULT 11
CK260235      765 bp mRNA linear EST 03-AUG-2004
LOCUS      EST706313 potato abiotic stress cDNA library Solanum tuberosum cDNA
DEFINITION      clone POAB294 3' end, mRNA sequence.
ACCESSION      CK260235
VERSION        CK260235.1 GI:39817213
KEYWORDS       EST.
SOURCE         Solanum tuberosum (potato)
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE
AUTHORS      Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE        Generation of ESTs from abiotic stressed potato tissue
JOURNAL      Unpublished (2003)
COMMENT      Other ESTs: EST706310 EST706311 EST706312
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

FEATURES
source
Location/Qualifiers
1..765
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAB294"
/tissue_type="abiotic stress treated leaf and root tissue"
/clone_lib="potato abiotic stress cDNA library"
/clone_vector="pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d, and 4d were grown under the standard conditions
and then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN
Query Match      67.6%; Score 19.6; DB 7; Length 790;
Best Local Similarity 84.6%; Pred. No. 4.3e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3  GTCAGAGGTTACCATAGGCCACTAG 28
          |||||
          669  GTCAGAGGTTGCTTTTGAGCCACTAG 694

Db

RESULT 12
CK260232      790 bp mRNA linear EST 03-AUG-2004
LOCUS      EST706310 potato abiotic stress cDNA library Solanum tuberosum cDNA
DEFINITION      clone POAB294 3' end, mRNA sequence.
ACCESSION      CK260232
VERSION        CK260232.1 GI:39817210
KEYWORDS       EST.
SOURCE         Solanum tuberosum (potato)
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE
AUTHORS      Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE        Generation of ESTs from abiotic stressed potato tissue
JOURNAL      Unpublished (2003)
COMMENT      Other ESTs: EST706311 EST706312 EST706313
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: TGT AAA ACG ACG GCC AGT.

FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAB294"
/tissue_type="abiotic stress treated leaf and root tissue"
/clone_lib="potato abiotic stress cDNA library"
/clone_vector="pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d, and 4d were grown under the standard conditions
and then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN
Query Match      67.6%; Score 19.6; DB 7; Length 765;
Best Local Similarity 84.6%; Pred. No. 4.2e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3  GTCAGAGGTTACCATAGGCCACTAG 28
          |||||
          669  GTCAGAGGTTGCTTTTGAGCCACTAG 694

Db

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RESULT 13
DE114072
LOCUS
DEFINITION
Oryzias latipes DNA, forward end of BAC clone: Md0158G03, genomic
survey sequence.
ACCESSION
DE114072
VERSION
DE114072.1 GI:71633484
KEYWORDS
GSS.
SOURCE
Oryzias latipes (Japanese medaka)
ORGANISM
Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE
1 Shimizu N., Asakawa, S., Shimizu, A. and Sasaki, T.
The BAC end sequence of Oryzias latipes
Published Only in Database (2005)
2 (bases 1 to 803)
Shimizu, N., Asakawa, S., Sasaki, T. and Shimizu, A.
Direct Submission
Submitted (30-JUN-2005) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku,
Tokyo, 160-8582, Japan (E-mail: nshimizu@db.med.keio.ac.jp,
Tel: 81-3-3351-2370, Fax: 81-3-3351-2370)
Location/Qualifiers
1 .803
/organism="Oryzias latipes"
/mol_type="genomic DNA"
/db_xref="taxon:8090"
/clone="Md0158G03"
/clone_lib="Medaka HdrR BAC library"
/notes="This sequence is forward end of BAC clone
Md0158G03."
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Query Match 67.6%; Score 19.6; DB 11; Length 803;
Best Local Similarity 84.6%; Pred. No. 4.3e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCCTCAGAGTTACCATAGGCCACT 26
Db 289 GAGTCAGTGGTTCCATAGAGACACT 314

RESULT 14
CR099508
LOCUS
DEFINITION
Forward strand read from insert in 3'HPT insertion targeting and
chromosome engineering clone MHPP279f02, genomic survey sequence.
ACCESSION
CR099508
VERSION
CR099508.1 GI:49846907
KEYWORDS
GSS; genome survey sequence; MICR.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 838)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR
Location/Qualifiers
1..838
/organism="Mus musculus"
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/db_xref="taxon:10090"
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Query Match 67.6%; Score 19.6; DB 11; Length 838;
Best Local Similarity 84.6%; Pred. No. 4.3e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CTCAGAGTTACCATAGGCCACTAG 28
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Search completed: March 5, 2006, 23:58:01
Job time : 3171 secs

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ORIGIN
Query Match 67.6%; Score 19.6; DB 11; Length 838;
Best Local Similarity 84.6%; Pred. No. 4.3e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 TCAGAGTTACCATAGGCCACTAGG 29
Db 628 TCTGTGGTTACCACAGCGCGTAGG 653

RESULT 15
CL110457
LOCUS
DEFINITION
ISBI-53J18 T7.1 ISBI Xenopus tropicalis genomic clone ISBI-53J18,
genomic survey sequence.
ACCESSION
CL110457
VERSION
CL110457.1 GI:40604092
KEYWORDS
GSS.
SOURCE
Xenopus tropicalis (western clawed frog)
ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE
1 (bases 1 to 990)
Kremitski, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence start: 75
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:8364"
/clone="ISBI-53J18"
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/notes="Vector: pBelOBAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"
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Best Local Similarity 84.6%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CTCAGAGTTACCATAGGCCACTAG 28
Db 755 GTAAGATGATACCATAGGCCACTAG 780

Search completed: March 5, 2006, 23:58:01
Job time : 3171 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 19:08:04 ; Search time 80.5 Seconds  
(without alignments)  
640.364 Million cell updates/sec

Title: US-10-720-424B-8

Perfect score: 29  
Sequence: 1 ggcgtcagaggtaccatagagccactagg 29

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/H COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/ECTUS COMB.seq.\*  
7: /cgn2\_6/prodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/prodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	24.2	83.4	1494	3	US-09-413-611A-5
C 3	24.2	83.4	1500	3	US-09-413-611A-7
C 4	24.2	83.4	1517	2	US-08-032-869A-1
C 5	24.2	83.4	1517	2	US-08-032-869A-2
C 6	24.2	83.4	1517	2	US-08-472-673-1
C 7	24.2	83.4	1517	2	US-08-472-673-2
C 8	24.2	83.4	1517	2	US-08-475-782-1
C 9	24.2	83.4	1517	2	US-08-475-782-2
C 10	24.2	83.4	1517	2	US-08-472-678-1
C 11	24.2	83.4	1517	2	US-08-472-678-2
C 12	24.2	83.4	1517	2	US-08-484-503-1
C 13	24.2	83.4	1517	2	US-08-484-503-2
C 14	24.2	83.4	1518	3	US-08-944-368A-1
C 15	24.2	83.4	1518	3	US-09-820-764-1
C 16	24.2	83.4	1518	3	US-09-886-118-1
C 17	24.2	83.4	1518	3	US-09-824-017-1
C 18	24.2	83.4	7904	2	US-08-316-239B-1
C 19	24.2	83.4	7904	2	US-08-316-239B-2
C 20	24.2	83.4	7904	2	US-08-410-005-1
C 21	24.2	83.4	7904	2	US-08-929-140-1
C 22	24.2	83.4	7904	3	US-09-560-579A-1
C 23	24.2	83.4	7917	2	US-08-167-854-1
C 24	22.8	78.6	383	3	US-09-319-056B-10

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C 26	22.6	77.9	647	3	US-08-578-634C-1	Sequence 1, Appli
C 27	22.6	77.9	647	3	US-09-430-010-1	Sequence 1, Appli
C 28	22.6	77.9	1518	2	US-08-815-667-8	Sequence 8, Appli
C 29	22.6	77.9	1524	2	US-08-409-122-1	Sequence 1, Appli
C 30	22.6	77.9	1524	2	US-08-408-669-1	Sequence 1, Appli
C 31	22.6	77.9	1524	3	US-08-913-644-1	Sequence 1, Appli
C 32	21	72.4	386	3	US-09-319-056B-13	Sequence 13, Appl
C 33	21	72.4	386	3	US-09-319-056B-15	Sequence 15, Appl
C 34	21	72.4	386	3	US-09-319-056B-16	Sequence 16, Appl
C 35	21	72.4	386	3	US-09-319-056B-18	Sequence 18, Appl
C 36	21	72.4	1518	2	US-08-815-667-9	Sequence 9, Appli
C 37	21	72.4	1518	2	US-08-815-667-13	Sequence 13, Appl
C 38	19.6	67.6	398	3	US-09-000-266-28	Sequence 28, Appl
C 39	19.6	67.6	398	3	US-09-000-266-30	Sequence 30, Appl
C 40	19.6	67.6	398	3	US-09-628-099-28	Sequence 28, Appl
C 41	19.6	67.6	398	3	US-09-628-099-30	Sequence 30, Appl
C 42	19.6	67.6	398	3	US-10-056-360-28	Sequence 28, Appl
C 43	19.6	67.6	398	3	US-10-056-360-30	Sequence 30, Appl
C 44	19.6	67.6	398	3	US-10-056-359-28	Sequence 28, Appl
C 45	19.6	67.6	398	3	US-10-056-359-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-09-210-168-2/c  
; Sequence 2, Application US/09210168  
; Patent No. 6355424  
; GENERAL INFORMATION:  
; APPLICANT: Lorincz, Attila T.  
; TITLE OF INVENTION: ASSESSMENT OF HUMAN PAPILLOMA VIRUS-RELATED DISEASE  
; FILE REFERENCE: 26294005US2  
; CURRENT APPLICATION NUMBER: US/09/210,168  
; CURRENT FILING DATE: 1998-12-11  
; PRIOR APPLICATION NUMBER: U.S. 60/082,167  
; PRIOR FILING DATE: 1998-04-17  
; PRIOR APPLICATION NUMBER: U.S. 60/070,486  
; PRIOR FILING DATE: 1998-01-05  
; PRIOR APPLICATION NUMBER: U.S. 60/069,426  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1484  
; TYPE: DNA  
; ORGANISM: Human papillomavirus  
; FEATURE:  
; OTHER INFORMATION: L1-HPV16  
US-09-210-168-2

Query Match 83.4%; Score 24.2; DB 3; Length 1484;

Best Local Similarity 89.7%; Pred. No. 0.076; Mismatches 0; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29

DB 890 GCATCAGAGGTTACCATAGACCACTAGG 862

RESULT 2

US-09-413-611A-5/c  
; Sequence 5, Application US/09413611A  
; Patent No. 6380364  
; GENERAL INFORMATION:  
; APPLICANT: Mueller, Martin  
; APPLICANT: Kast, Wilbe  
; APPLICANT: Nieland, John  
; APPLICANT: Velders, Markwin  
; TITLE OF INVENTION: Chimeric Biotin-Binding Papillomavirus Protein  
; FILE REFERENCE: 202325  
; CURRENT APPLICATION NUMBER: US/09/413,611A

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; CURRENT FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 60/109,510
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:biotin-binding
; OTHER INFORMATION: papillomavirus protein 168
; NAME/KEY: CDS
; LOCATION: (1)..(1491)
; US-09-413-611A-5

Query Match      83.4%; Score 24.2; DB 3; Length 1494;
Best Local Similarity 89.7%; Pred. No. 0.076;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 911 GCATCAGAGGTAACCATAGAACCACTAGG 883

RESULT 3
US-09-413-611A-7/c
; Sequence 7, Application US/09413611A
; Patent No. 6380364
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Kast, Wjbe
; APPLICANT: Nieland, John
; APPLICANT: Velders, Markwin
; TITLE OF INVENTION: Chimeric Biotin-Binding Papillomavirus Protein
; FILE REFERENCE: 202325
; CURRENT APPLICATION NUMBER: US/09/413,611A
; CURRENT FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 60/109,510
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:biotin-binding
; OTHER INFORMATION: papillomavirus protein 169
; NAME/KEY: CDS
; LOCATION: (1)..(1497)
; US-09-413-611A-7

Query Match      83.4%; Score 24.2; DB 3; Length 1500;
Best Local Similarity 89.7%; Pred. No. 0.076;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCAGAGGTTACCATAGAGCCACTAGG 29
   ||||||| ||||||| ||||||| |||||||
Db 911 GCATCAGAGGTAACCATAGAACCACTAGG 883

RESULT 4
US-08-032-869A-1/c
; Sequence 1, Application US/08032869A
; Patent No. 5437951
; GENERAL INFORMATION:
; APPLICANT: Lowy, Douglas R.
; APPLICANT: Schiller, John T.
; APPLICANT: Kirnbauer, Reinhard
; TITLE OF INVENTION: SELF-ASSEMBLING RECOMBINANT
; TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS
; NUMBER OF SEQUENCES: 6
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/032,869A
; FILING DATE: 16-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,371
; FILING DATE: 03-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirkpatrick Ph.D., Anita M.
; REGISTRATION NUMBER: 32,617
; REFERENCE/DOCKET NUMBER: NIH032.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human papillomavirus
; STRAIN: HPV16
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1517
; US-08-032-869A-1

Query Match      83.4%; Score 24.2; DB 2; Length 1517;
Best Local Similarity 89.7%; Pred. No. 0.076;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCTCAGAGGTTACCATAGAGCCACTAGG 29
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Db 911 GCATCAGAGGTAACCATAGAACCACTAGG 883

RESULT 5
US-08-032-869A-2/c
; Sequence 2, Application US/08032869A
; Patent No. 5437951
; GENERAL INFORMATION:
; APPLICANT: Lowy, Douglas R.
; APPLICANT: Schiller, John T.
; APPLICANT: Kirnbauer, Reinhard
; TITLE OF INVENTION: SELF-ASSEMBLING RECOMBINANT
; TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1517
US-08-472-673-2

Query Match      83.4%; Score 24.2; DB 2; Length 1517;
Best Local Similarity 89.7%; Pred. No. 0.076; 3; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db 911 GCATCAGAGGTAACCATAGAGCCACTAGG 883

RESULT 8
US-08-475-782-1/c
; Sequence 1, Application US/08475782
; Patent No. 5744142
; GENERAL INFORMATION:
; APPLICANT: Lowy, Douglas R.
; APPLICANT: Schiller, John T.
; APPLICANT: Kirnbauer, Reinhard
; TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
; TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,782
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/032,869
; FILING DATE: 16-MAR-1993
; APPLICATION NUMBER: US 07/941,371
; FILING DATE: 03-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirkpatrick Ph.D., Anita M.
; REGISTRATION NUMBER: 32,617
; REFERENCE/DOCKET NUMBER: NIH032.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human papillomavirus
; STRAIN: HPV16
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: 1..1517
US-08-475-782-1

Query Match      83.4%; Score 24.2; DB 2; Length 1517;
Best Local Similarity 89.7%; Pred. No. 0.076; 3; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db 911 GCATCAGAGGTAACCATAGAGCCACTAGG 883

RESULT 9
US-08-475-782-2/c
; Sequence 2, Application US/08475782
; Patent No. 5744142
; GENERAL INFORMATION:
; APPLICANT: Lowy, Douglas R.
; APPLICANT: Schiller, John T.
; APPLICANT: Kirnbauer, Reinhard
; TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
; TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,782
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/032,869
; FILING DATE: 16-MAR-1993
; APPLICATION NUMBER: US 07/941,371
; FILING DATE: 03-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirkpatrick Ph.D., Anita M.
; REGISTRATION NUMBER: 32,617
; REFERENCE/DOCKET NUMBER: NIH032.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; LOCATION: 1..1517
US-08-475-782-2

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Best Local Similarity 89.7%; Pred. No. 0.076; 3; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db 911 GCATCAGAGGTAACCATAGAGCCACTAGG 883
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; Sequence 1, Application US/08472678  
; Patent No. 5871998  
; GENERAL INFORMATION:  
; APPLICANT: Lowy, Douglas R.  
; APPLICANT: Schiller, John T.  
; APPLICANT: Kirmbaurer, Reinhard  
; TITLE OF INVENTION: SELF-ASSEMBLING RECOMBINANT  
; TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR  
; STREET: 620 Newport Center Drive, Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,678  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/032,869A  
; FILING DATE: 16-MAR-1993  
; APPLICATION NUMBER: US 07/941,371  
; FILING DATE: 03-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kirkpatrick Ph.D., Anita M.  
; REGISTRATION NUMBER: 32,617  
; REFERENCE/DOCKET NUMBER: NIH032.001CPI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1517 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Human papillomavirus  
; STRAIN: HPV16  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1517  
US-08-472-678-1  
Query Match 83.4%; Score 24.2; DB 2; Length 1517;  
Best Local Similarity 89.7%; Pred. No. 0.076;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29  
DB 911 GCATCAGAGGTTACCATAGAGCCACTAGG 883  
RESULT 11  
US-08-472-678-2/c  
; Sequence 2, Application US/08472678  
; Patent No. 5871998  
; GENERAL INFORMATION:  
; APPLICANT: Lowy, Douglas R.  
; APPLICANT: Schiller, John T.

; APPLICANT: Kirmbaurer, Reinhard  
; TITLE OF INVENTION: SELF-ASSEMBLING RECOMBINANT  
; TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR  
; STREET: 620 Newport Center Drive, Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
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; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/032,869A  
; FILING DATE: 16-MAR-1993  
; APPLICATION NUMBER: US 07/941,371  
; FILING DATE: 03-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kirkpatrick Ph.D., Anita M.  
; REGISTRATION NUMBER: 32,617  
; REFERENCE/DOCKET NUMBER: NIH032.001CPI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1517 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
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; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1517  
US-08-472-678-2  
Query Match 83.4%; Score 24.2; DB 2; Length 1517;  
Best Local Similarity 89.7%; Pred. No. 0.076;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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DB 911 GCATCAGAGGTTACCATAGAGCCACTAGG 883  
RESULT 12  
US-08-484-503-1/c  
; Sequence 1, Application US/08484503  
; Patent No. 5985610  
; GENERAL INFORMATION:  
; APPLICANT: Lowy, Douglas R.  
; APPLICANT: Schiller, John T.  
; APPLICANT: Kirmbaurer, Reinhard  
; TITLE OF INVENTION: SELF-ASSEMBLING RECOMBINANT  
; TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR  
; STREET: 620 Newport Center Drive, Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,503
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/032,869
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirkpatrick Ph.D., Anita M.
; REGISTRATION NUMBER: 32,617
; REFERENCE/DOCKET NUMBER: NIH032.001CPI
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human papillomavirus
; STRAIN: HPV16
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1517
; US-08-484-503-1

Query Match 83.4%; Score 24.2; DB 2; Length 1517;
Best Local Similarity 89.7%; Pred. No. 0.076;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 911 GCATCAGAGGTAACCATAGACCCTAGG 883

RESULT 13
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; Sequence 2, Application US/08484503
; Patent No. 5985610
; GENERAL INFORMATION:
; APPLICANT: Lowy, Douglas R.
; APPLICANT: Schiller, John T.
; APPLICANT: Kirnbauer, Reinhard
; TITLE OF INVENTION: SELF-ASSEMBLING RECOMBINANT
; TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,503
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/032,869
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirkpatrick Ph.D., Anita M.
; REGISTRATION NUMBER: 32,617
; REFERENCE/DOCKET NUMBER: NIH032.001CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1517
; US-08-484-503-2

Query Match 83.4%; Score 24.2; DB 2; Length 1517;
Best Local Similarity 89.7%; Pred. No. 0.076;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGGCCACTAGG 29
Db 911 GCATCAGAGGTAACCATAGACCCTAGG 883

RESULT 14
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; Sequence 1, Application US/08944368A
; Patent No. 6228368
; GENERAL INFORMATION:
; APPLICANT: Glasman, et al.
; TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
; TITLE OF INVENTION: Formulations and Methods of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,368A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27013/34028
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1518 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: 1..1518
US-08-944-368A-1

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Best Local Similarity 89.7%; Pred. No. 0.076; 3; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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DB 911 GCATCAGAGGTAACCATAGAGCCACTAGG 883

RESULT 15
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; Sequence 1, Application US/09820764
; Patent No. 6352696
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/820,764
; APPLICATION NUMBER: US/09/820,764
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercok, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1518 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
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; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-820-764-1

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Best Local Similarity 89.7%; Pred. No. 0.076; 3; Indels 0; Gaps 0;
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QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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DB 911 GCATCAGAGGTAACCATAGAGCCACTAGG 883

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Search completed: March 5, 2006, 19:13:35  
Job time : 80.5 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:00:24 ; Search time 361 Seconds  
(without alignments)  
664.299 Million cell updates/sec

Title: US-10-720-424B-8  
Perfect score: 29  
Sequence: 1 ggcgcagaggttaccatagcactagg 29

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134699005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA\_Main:\*

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- 3: /cgn2\_6/prodata/1/pubpna/US09A\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	24.2	83.4	1452	9	US-10-487-719-2
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4	24.2	83.4	1484	3	US-09-970-477-2
5	24.2	83.4	1517	3	US-09-832-065-1
6	24.2	83.4	1517	3	US-09-832-065-2
7	24.2	83.4	1517	6	US-10-371-846-1
8	24.2	83.4	1517	6	US-10-371-846-2
9	24.2	83.4	1518	3	US-09-820-765-1
10	24.2	83.4	1518	3	US-09-162-904A-1
11	24.2	83.4	1518	3	US-09-162-904A-2
12	24.2	83.4	1518	3	US-09-824-017-1
13	24.2	83.4	1518	3	US-09-986-118A-1
14	24.2	83.4	1518	6	US-10-367-095-11
15	24.2	83.4	1518	6	US-10-367-095-12
16	24.2	83.4	1518	7	US-10-368-046-11
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23	24.2	83.4	1518	9	US-10-487-719-3

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Sequence 15, App  
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Sequence 38, Appl  
Sequence 20, Appl  
Sequence 17310, A  
Sequence 7, Appl  
Sequence 3, Appl  
Sequence 68, Appl  
Sequence 661735,  
Sequence 661736,  
Sequence 498, App

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US-10-433-091-1  
US-10-978-233-14  
US-10-720-424B-9  
US-10-087-192-450  
US-09-925-065A-151425  
US-10-367-057-127  
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US-10-056-360-28  
US-10-056-360-30  
US-10-779-543-17310  
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US-09-925-065A-661736  
US-10-322-281-498

ALIGNMENTS

RESULT 1  
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; Sequence 8, Application US/10720424B  
; Publication No. US20040248085A1  
; GENERAL INFORMATION:  
; APPLICANT: ALBIOMED CO., LTD  
; APPLICANT: Lee, Sang-Wha  
; APPLICANT: Kim, Yeon-Soo  
; APPLICANT: Yu, Kang-Yeol  
; APPLICANT: Kim, Seung-Jo  
; APPLICANT: Cha, Kwang-Yul  
; APPLICANT: Ko, Jung-Jae  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR  
; FILE REFERENCE: NEI70018  
; CURRENT APPLICATION NUMBER: US/10/720,424B  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: KR10-2002-0075370  
; PRIOR FILING DATE: 2002-11-29  
; PRIOR APPLICATION NUMBER: KR10-2003-0053147  
; PRIOR FILING DATE: 2003-07-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Human Papillomavirus  
US-10-720-424B-8

Query Match 100.0%; Score 29; DB 8; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.00072; Mismatches 0; Indels 0; Gaps 0;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCGTCAGAGGTTACCATAGGCACTAGG 29  
Db 1 GCGTCAGAGGTTACCATAGGCACTAGG 29

RESULT 2  
US-10-487-719-2/c  
; Sequence 2, Application US/10487719  
; Publication No. US20050090435A1  
; GENERAL INFORMATION:  
; APPLICANT: Varsani, Arvind  
; APPLICANT: Tybicki, Edward  
; APPLICANT: Williamson, Anna-Lise



STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Human papillomavirus  
STRAIN: HPV16  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1517  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-832-065-1

Query Match 83.4%; Score 24.2; DB 3; Length 1517;  
Best Local Similarity 89.7%; Pred. No. 0.25;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29  
DB 911 GCATCAGAGGTAACCATAGAGCCACTAGG 883

RESULT 6  
US-09-832-065-2/c  
; Sequence 2, Application US/09832065  
; Publication No. US20030050439A1  
; GENERAL INFORMATION:  
; APPLICANT: Lowy, Douglas R.  
; Schiller, John T.  
; Kirnbauer, Reinhard  
; TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT  
; PAPILLOMAVIRUS CAPSID PROTEINS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR  
; STREET: 620 Newport Center Drive, Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/09/832,065  
; FILING DATE: 09-Apr-2001  
; CLASSIFICATION: <Unknown>  
; APPLICATION NUMBER: 09/316,487  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kirkpatrick Ph.D., Anita M.  
; REGISTRATION NUMBER: 32,617  
; REFERENCE/DOCKET NUMBER: NIH032.001CP1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1517 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1517  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-832-065-2  
Query Match 83.4%; Score 24.2; DB 3; Length 1517;  
Best Local Similarity 89.7%; Pred. No. 0.25;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29  
DB 911 GCATCAGAGGTAACCATAGAGCCACTAGG 883

RESULT 7  
US-10-371-846-1/c  
; Sequence 1, Application US/10371846  
; Publication No. US20030219873A1  
; GENERAL INFORMATION:  
; APPLICANT: Lowy, Douglas R.  
; Schiller, John T.  
; Kirnbauer, Reinhard  
; TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT  
; PAPILLOMAVIRUS CAPSID PROTEINS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR  
; STREET: 620 Newport Center Drive, Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/10/371,846  
; FILING DATE: 21-Feb-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/032,869  
; FILING DATE: 16-MAR-1993  
; APPLICATION NUMBER: US 07/941,371  
; FILING DATE: 03-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kirkpatrick Ph.D., Anita M.  
; REGISTRATION NUMBER: 32,617  
; REFERENCE/DOCKET NUMBER: NIH032.001CP1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1517 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Human papillomavirus  
; STRAIN: HPV16  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1517  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-371-846-1

Query Match 83.4%; Score 24.2; DB 6; Length 1517;  
Best Local Similarity 89.7%; Pred. No. 0.25;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29



LENGTH: 1518  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of L1 gene  
OTHER INFORMATION: HPV16 DNA clone P114/16/2  
US-09-162-904A-1

Query Match 83.4%; Score 24.2; DB 3; Length 1518;  
Best Local Similarity 89.7%; Pred. No. 0.25;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29  
DB 911 GCATCAGAGGTAACCATAGAGCCACTAGG 883

RESULT 11  
US-09-162-904A-2/c  
Sequence 2, Application US/09162904A  
Patent No. US20020168372A1.  
GENERAL INFORMATION:  
APPLICANT: Gissmann, Lutz  
TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE  
FILE REFERENCE: 8484-068-999  
CURRENT APPLICATION NUMBER: US/09/162,904A  
CURRENT FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 08/884,168  
PRIOR FILING DATE: 1997-06-27  
PRIOR APPLICATION NUMBER: 08/641,570  
PRIOR FILING DATE: 1996-05-01  
PRIOR APPLICATION NUMBER: 08/902,528  
PRIOR FILING DATE: 1993-07-16  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 2  
LENGTH: 1518  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of L1 gene  
OTHER INFORMATION: HPV16 DNA clone P114/16/11  
US-09-162-904A-2

Query Match 83.4%; Score 24.2; DB 3; Length 1518;  
Best Local Similarity 89.7%; Pred. No. 0.25;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29  
DB 911 GCATCAGAGGTAACCATAGAGCCACTAGG 883

RESULT 12  
US-09-824-017-1/c  
Sequence 1, Application US/09824017  
Publication No. US20020197668A1  
GENERAL INFORMATION:  
APPLICANT: BURGER, Alexander  
HALLER, Michael  
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
FORMULATIONS AND METHODS OF USE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/824,017  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/026,896  
FILING DATE: 1998-02-20  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1518 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1515  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-824-017-1

Query Match 83.4%; Score 24.2; DB 3; Length 1518;  
Best Local Similarity 89.7%; Pred. No. 0.25;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29  
DB 911 GCATCAGAGGTAACCATAGAGCCACTAGG 883

RESULT 13  
US-09-986-118A-1/c  
Sequence 1, Application US/09986118A  
Publication No. US20030021806A1  
GENERAL INFORMATION:  
APPLICANT: BURGER, Alexander  
HALLER, Michael  
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
FORMULATIONS AND METHODS OF USE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/986,118A  
FILING DATE: 07-No. US20030021806A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/026,896  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102



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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:06:14 ; Search time 457 Seconds  
(without alignments)  
139.129 Million cell updates/sec

Title: US-10-720-424B-8

Perfect score: 29  
Sequence: 1 gcgtcagaggtaccatagaccactagg 29.

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

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Listing first 45 summaries

Database : Published Applications NA\_New.\*

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- 8: /cgn2\_6/ptodata/1/pubnpna/US10\_NEW\_PUB.seq1.\*
- 9: /cgn2\_6/ptodata/1/pubnpna/US11\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubnpna/US11\_NEW\_PUB.seq1.\*
- 11: /cgn2\_6/ptodata/1/pubnpna/US11\_NEW\_PUB.seq2.\*
- 12: /cgn2\_6/ptodata/1/pubnpna/US11\_NEW\_PUB.seq3.\*
- 13: /cgn2\_6/ptodata/1/pubnpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24.2	83.4	1518	7 US-10-514-878A-2	Sequence 2, Appli
C 2	24.2	83.4	1518	7 US-10-514-878A-4	Sequence 4, Appli
C 3	24.2	83.4	1518	7 US-10-514-878A-6	Sequence 6, Appli
C 4	24.2	83.4	1518	7 US-10-514-878A-8	Sequence 8, Appli
C 5	24.2	83.4	1518	7 US-10-514-878A-10	Sequence 10, Appli
C 6	24.2	83.4	1518	7 US-10-514-878A-12	Sequence 12, Appli
C 7	24.2	83.4	1518	12 US-11-179-478-1	Sequence 1, Appli
C 8	20.2	69.7	421	6 US-09-925-065A-151425	Sequence 151425,
C 9	18.8	64.8	567	6 US-09-925-065A-661735	Sequence 661735,
C 10	18.8	64.8	567	6 US-09-925-065A-661736	Sequence 661736,
C 11	18	62.1	541	6 US-09-925-065A-13399	Sequence 13399, A
C 12	18	62.1	541	6 US-09-925-065A-13400	Sequence 13400, A
C 13	18	62.1	586	6 US-09-925-065A-537693	Sequence 537693,
C 14	18	62.1	645	6 US-09-925-065A-727186	Sequence 727186,
C 15	18	62.1	1021	8 US-10-750-185-31766	Sequence 31766, A
C 16	18	62.1	1021	8 US-10-750-185-31766	Sequence 31766, A
C 17	18	62.1	2457	12 US-11-128-061-800	Sequence 800, App
C 18	18	62.1	2457	12 US-11-128-049-800	Sequence 800, App
C 19	17.8	61.4	201	8 US-10-995-561-27379	Sequence 27379, A
C 20	17.8	61.4	201	8 US-10-995-561-42693	Sequence 42693, A

C 21	17.8	61.4	201	12 US-11-124-367A-14923	Sequence 14923, A
C 22	17.8	61.4	201	12 US-11-124-367A-33222	Sequence 33222, A
C 23	17.8	61.4	563	6 US-09-925-065A-689088	Sequence 689088,
C 24	17.8	61.4	563	6 US-09-925-065A-689089	Sequence 689089,
C 25	17.8	61.4	53641	8 US-10-995-561-13238	Sequence 13238, A
C 26	17.8	61.4	1125000	8 US-10-995-561-13286	Sequence 13286, A
C 27	17.6	60.7	814	6 US-09-925-065A-54678	Sequence 54678, A
C 28	17.6	60.7	1753	8 US-10-750-185-35843	Sequence 35843, A
C 29	17.6	60.7	1753	8 US-10-750-623-35843	Sequence 35843, A
C 30	17.6	60.7	2129	8 US-09-925-065A-709891	Sequence 709891,
C 31	17.6	60.7	3045	8 US-10-750-185-59924	Sequence 59924, A
C 32	17.6	60.7	3045	8 US-10-750-623-59924	Sequence 59924, A
C 33	17.4	60.0	449	6 US-09-925-065A-796428	Sequence 796428,
C 34	17.4	60.0	449	6 US-09-925-065A-851486	Sequence 851486,
C 35	17.4	60.0	454	6 US-09-925-065A-796346	Sequence 796346,
C 36	17.4	60.0	454	6 US-09-925-065A-851448	Sequence 851448,
C 37	17.4	60.0	522	6 US-09-925-065A-274631	Sequence 274631,
C 38	17.4	60.0	525	6 US-09-925-065A-411761	Sequence 411761,
C 39	17.4	60.0	525	6 US-09-925-065A-411762	Sequence 411762,
C 40	17.4	60.0	526	6 US-09-925-065A-391311	Sequence 391311,
C 41	17.4	60.0	535	6 US-09-925-065A-99734	Sequence 99734, A
C 42	17.4	60.0	564	6 US-09-925-065A-103917	Sequence 103917,
C 43	17.4	60.0	587	6 US-09-925-065A-301382	Sequence 301382,
C 44	17.4	60.0	599	6 US-09-925-065A-301381	Sequence 301381,
C 45	17.4	60.0	604	6 US-09-925-065A-301380	Sequence 301380,

#### ALIGNMENTS

##### RESULT 1

US-10-514-878A-2/c

; Sequence 2, Application US/10514878A

; Publication No. US20060035319A1

; GENERAL INFORMATION:

; APPLICANT: University of Cape Town

; TITLE OF INVENTION: Chimeric Human Papillomavirus 16 L1 Virus-Like Particles and Met

; FILE REFERENCE: 10/514,878

; CURRENT APPLICATION NUMBER: US/10/514,878A

; CURRENT FILING DATE: 2004-11-16

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 1518

; TYPE: DNA

; ORGANISM: Human papillomavirus

US-10-514-878A-2

Query Match

Best Local Similarity 83.4%; Score 24.2; DB 7; Length 1518;

Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTACCATAGACCCTAGG 29

DB 911 GCATCAGAGGTAACCATAGAACCTAGG 883

##### RESULT 2

US-10-514-878A-4/c

; Sequence 4, Application US/10514878A

; Publication No. US20060035319A1

; GENERAL INFORMATION:

; APPLICANT: University of Cape Town

; TITLE OF INVENTION: Chimeric Human Papillomavirus 16 L1 Virus-Like Particles and Met

; FILE REFERENCE: 10/514,878

; CURRENT APPLICATION NUMBER: US/10/514,878A

; CURRENT FILING DATE: 2004-11-16

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 1518

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; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-4

Query Match      83.4%; Score 24.2; DB 7; Length 1518;
Best Local Similarity 89.7%; Pred. No. 0.066;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
   ||||||| ||||||| ||||||| |||||||
Db 911 GCATCAGAGGTAACCATAGAACCACTAGG 883

RESULT 3
US-10-514-878A-6/c
; Sequence 6, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Methods of Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-6

Query Match      83.4%; Score 24.2; DB 7; Length 1518;
Best Local Similarity 89.7%; Pred. No. 0.066;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
   ||||||| ||||||| ||||||| |||||||
Db 911 GCATCAGAGGTAACCATAGAACCACTAGG 883

RESULT 4
US-10-514-878A-8/c
; Sequence 8, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Methods of Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-8

Query Match      83.4%; Score 24.2; DB 7; Length 1518;
Best Local Similarity 89.7%; Pred. No. 0.066;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
   ||||||| ||||||| ||||||| |||||||
Db 911 GCATCAGAGGTAACCATAGAACCACTAGG 883

RESULT 5
US-10-514-878A-10/c
; Sequence 10, Application US/10514878A
; Publication No. US20060035319A1
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; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Methods of Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-10

Query Match      83.4%; Score 24.2; DB 7; Length 1518;
Best Local Similarity 89.7%; Pred. No. 0.066;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
   ||||||| ||||||| ||||||| |||||||
Db 911 GCATCAGAGGTAACCATAGAACCACTAGG 883

RESULT 6
US-10-514-878A-12/c
; Sequence 12, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Methods of Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-12

Query Match      83.4%; Score 24.2; DB 7; Length 1518;
Best Local Similarity 89.7%; Pred. No. 0.066;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
   ||||||| ||||||| ||||||| |||||||
Db 911 GCATCAGAGGTAACCATAGAACCACTAGG 883

RESULT 7
US-11-179-478-1/c
; Sequence 1, Application US/11179478
; Publication No. US20050249745A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; TITLE OF INVENTION: FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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QY 3 GTCAGAGGTTACCATAGAGCCA 24  
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Db 383 GTCAGAGGTCACCATGGAGCCA 404

RESULT 11  
US-09-925-065A-13399  
; Sequence 13399, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13399  
; LENGTH: 541  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-13399

Query Match 62.1%; Score 18; DB 6; Length 541;  
Best Local Similarity 80.8%; Pred. No. 57;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TCGAGGTTACCATAGAGCCACTAGG 29  
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Db 262 TCAGAGGATCGAGTACAGAGCACTAGG 287

RESULT 12  
US-09-925-065A-13400  
; Sequence 13400, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13400  
; LENGTH: 541  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-13400

Query Match 62.1%; Score 18; DB 6; Length 541;

Best Local Similarity 80.8%; Pred. No. 57;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 4 TCGAGGTTACCATAGAGCCACTAGG 29  
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Db 262 TCAGAGGATCGAGTACAGAGCACTAGG 287

RESULT 13  
US-09-925-065A-537693  
; Sequence 537693, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 537693  
; LENGTH: 586  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-537693

Query Match 62.1%; Score 18; DB 6; Length 586;  
Best Local Similarity 80.8%; Pred. No. 58;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CGTCAGAGGTTACCATAGAGCCACTA 27  
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Db 8 CCTCAGAGGATCCTCAGAGTCACTA 33

RESULT 14  
US-09-925-065A-727186/c  
; Sequence 727186, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 727186  
; LENGTH: 645  
; TYPE: DNA  
; ORGANISM: Homo sapiens

Search completed: March 5, 2006, 22:37:01  
Job time : 458 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:52:50 ; Search time 907 Seconds  
(without alignments)  
1817.486 Million cell updates/sec

Title: US-10-720-424B-8

Perfect score: 29  
Sequence: 1 ggcgtcaggggtaccatagagccactagg 29

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_in:\*

3: gb\_env:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pr:\*

9: gb\_ro:\*

10: gb\_stc:\*

11: gb\_sv:\*

12: gb\_un:\*

13: gb\_vi:\*

14: gb\_hcg:\*

15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25.8	89.0	803	13	DQ003071 Human pap
C 2	25.8	89.0	7851	13	M74117 Human papil
C 3	25.8	89.0	7852	13	X74474 Human papil
C 4	25.8	89.0	7879	13	X74477 Human papil
C 5	24.4	84.1	7759	13	U37488 Human papil
C 6	24.4	84.1	7904	13	AF293961 Human pap
C 7	24.2	83.4	624	13	AY098925 Human pap
C 8	24.2	83.4	635	13	AY098921 Human pap
C 9	24.2	83.4	667	13	AY098926 Human pap
C 10	24.2	83.4	799	13	DQ003067 Human pap
C 11	24.2	83.4	1257	13	AF512011 Human pap
C 12	24.2	83.4	1452	6	AX770809 Sequence
C 13	24.2	83.4	1452	6	AX770811 Sequence
C 14	24.2	83.4	1484	6	AR199234 Sequence
C 15	24.2	83.4	1484	13	U34165 Human papil
C 16	24.2	83.4	1484	13	U34166 Human papil
C 17	24.2	83.4	1484	13	U34167 Human papil
C 18	24.2	83.4	1484	13	U34168 Human papil

C 19	24.2	83.4	1484	13	HPU34169 Human papil
C 20	24.2	83.4	1484	13	HPU34171 Human papil
C 21	24.2	83.4	1484	13	HPU34172 Human papil
C 22	24.2	83.4	1484	13	HPU34173 Human papil
C 23	24.2	83.4	1484	13	HPU34174 Human papil
C 24	24.2	83.4	1484	13	HPU34175 Human papil
C 25	24.2	83.4	1484	13	HPU34176 Human papil
C 26	24.2	83.4	1484	13	HPU34177 Human papil
C 27	24.2	83.4	1484	13	HPU34178 Human papil
C 28	24.2	83.4	1484	13	HPU34179 Human papil
C 29	24.2	83.4	1484	13	HPU34180 Human papil
C 30	24.2	83.4	1484	13	HPU34181 Human papil
C 31	24.2	83.4	1484	13	HPU34182 Human papil
C 32	24.2	83.4	1484	13	HPU34183 Human papil
C 33	24.2	83.4	1484	13	HPU34184 Human papil
C 34	24.2	83.4	1484	13	HPU34185 Human papil
C 35	24.2	83.4	1484	13	HPU34186 Human papil
C 36	24.2	83.4	1484	13	HPU34187 Human papil
C 37	24.2	83.4	1484	13	HPU34188 Human papil
C 38	24.2	83.4	1484	13	HPU34189 Human papil
C 39	24.2	83.4	1484	13	HPU34190 Human papil
C 40	24.2	83.4	1484	13	HPU34191 Human papil
C 41	24.2	83.4	1484	13	HPU34192 Human papil
C 42	24.2	83.4	1484	13	HPU34193 Human papil
C 43	24.2	83.4	1486	13	AF003031 Human pap
C 44	24.2	83.4	1517	6	AR003253 Sequence
C 45	24.2	83.4	1517	6	AR003254 Sequence

## ALIGNMENTS

RESULT 1	DQ003071/c	DQ003071	803 bp	DNA	linear	VRL 15-AUG-2005
LOCUS	Human papillomavirus type 35	nonfunctional L1 gene, partial				
DEFINITION	sequence.					
ACCESSION	DQ003071					
VERSION	DQ003071.1	GI:66866327				
KEYWORDS	Human papillomavirus type 35					
SOURCE	Human papillomavirus type 35					
ORGANISM	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; Alphapapillomavirus.					
REFERENCE	1 (bases 1 to 803)					
AUTHORS	Wu, X., Ren, J., Ran, D. and Ma, R. Z.					
TITLE	Detection of HPV types in cervical brush samples of clinical patients in Beijing and other Northern China cities					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 803)					
AUTHORS	Wu, X., Ren, J. and Ma, R. Z.					
TITLE	Direct Submission					
JOURNAL	Submitted (08-APR-2005) Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, AS Datun Road, Chaoyang District, Beijing 100101, China					
FEATURES	Location/Qualifiers					
source	1..803					
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	/mol_type="genomic DNA"					
	/isolation_source="epithelial cells from cervix"					
	/sub_species="35"					
	/db_xref="taxon:10587"					
	/country="China"					
misc_feature	<1..>803					
	/note="nonfunctional L1 due to mutation"					
ORIGIN						
Query Match	89.0%;	Score 25.8;	DB 13;	Length 803;		
Best Local Similarity	93.1%;	Pred. No. 0.097;	Mismatches 2;	Indels 0;	Gaps 0;	
Matches	27;	Conservative 0;				
QY	1	CGGTCAGAGGTTACCATAGGCCACTAGG 29				

Db	799	GCATCGAGGTTACCATAGCCTAGG 771	CDS	562..861 /gene="E7" /note="putative" /codon_start=1 /product="transforming protein" /protein_id="AAA46967.1" /db_xref="GI:333052" /translation="MHGRIITLQDVVLDLEPATDLYCYEQLCDSSSEEDTIDGPAG QAKPDSNNYVTSCCKCEATLRLCVQSTHDIRKLEDLLMGTFTIVCPGCSQRA"
RESULT 2	PPH35CG	7851 bp DNA circular VRL 10-MAY-2002	gene	868..2760 /gene="E1" /note="putative" /codon_start=1 /product="replication protein" /protein_id="AAA46968.1" /db_xref="GI:333053" /translation="MADPAGTDEBGTGCGWFFVEAVVSRRTGSSVEDENDDCDRG EDWDFINDTILNQASTETAQALPHAQEOGTHKEAVQVLKRYKVASPSSVSLCVN NNISPLKAICENKNTAAKRLFELPSGCGNSEVEIHEIQVEGHDTVEQCSMGSG DSITSSDERHDETPTDIIQILKCSNANAAMAKFELFGISFTELIRFPKSKSTC TDMCVAFGIAPSVANFKHITYVIYVYRVHGAMVILALLFVKVEKREQQDKTIDAK LLCISAAGLIQPPKLRSTPAALYFKTAMNSISEVDGETPEWIORQTVLQHSFNDAI FDLSMVQWYDNDPIDDDIAYKVAQLAETNSACAFKNSQAKI VKDCATMGVPHY KRAEKREMTSQWIKRCAQYDDGDGMRDIVERFLYQQVDVAFLSALKNELHGVPKK NCILLYGAPNTCKSLFGMSLMHFLQCALISYVNSKSHFWLQDLYDAKMLDDATSPC GIYRPIFKKTRKWSYISFRCKALSIHVIMPTFTYIININAGKDRWPYLRKRVVFT FHNEPFDKNGNPEYGLNDKNMKSPFRTWCRNLNHEBEVKENDGDGAPFAFKCVSGQN TTRLRD"
LOCUS	M74117	GI:333050	CDS	2693..3796 /gene="E2" /note="putative" /codon_start=1 /product="regulatory protein" /protein_id="AAA46969.1" /db_xref="GI:333054" /translation="MMETLSQRLSVCQDKILHEHYETDSTCLSDHIQYWKILRLCAV YKAREMGIKTNHQVPTQALSKAKAMQALIELQMLELNTTEYDSTWLTQETSEL VTVPTCLCKDDVTVEAQDGDKONTWHTWTHIYLEDISICTVVKGLVNVKGIYY VHQVETYYVTFREAKYKGNIEWHVHGGVIVCPESVFSSTELSTAEIATQLHAY NITETHKACSVGTTEQKTNHRLRGTELPYNTKRVLSAVDSVGRGVSTSDCT NKDRGCSSTTPIVHLKGDANTLKCSRYLRKLYKALYQDASSTWRTCTNDKKQIAI VLTLYTYQRDKFLTIVKIPNTVTVSKGYMSI"
DEFINITION	Human papillomavirus type 35	complete genome.	gene	3273..3563 /gene="E4" /note="putative" /codon_start=1 /product="unknown" /protein_id="AAA46965.2" /db_xref="GI:20522255" /translation="MFVNLNLYLAQNYPLLKLLHSYTTTPRPPTPKPAPWAPQKPRR QITNDFEGVPSSPTTTPPSCDSVPWTVLTEGSTLHLTAQTKTGVVVVVVQLHL"
ACCESSION	M74117.1	GI:333050	CDS	3793..4038 /gene="E5" /note="putative" /codon_start=1 /product="transforming protein" /protein_id="AAA46966.1" /db_xref="GI:333051" /translation="MFQDPAERYKLHDLONEVEBSIHCNVCYCKQELQORSEYVD FACYDLCIVYGCQYGVCMCKLKFSKYRWRYSYVGETLEKQCNCQLCHLLIR CITCQKPLCFVEQRHLEKKRPHNIGRWTCRCMSCWKPTRRETEV"
VERSION	2	(bases 1 to 7851)	gene	405..416 /gene="E6" /standard_name="Splice donor"
KEYWORDS	complete genome; major capsid protein; minor capsid protein; regulatory protein; replication protein; transform protein.		gene	562..861 /gene="E7"
SOURCE	Human papillomavirus type 35			
ORGANISM	Human papillomavirus type 35			
REFERENCE	1	(sites)		
AUTHORS	Lorincz,A.T., Quinn,A.P., Lancaster,W.D. and Temple,G.P.			
TITLE	A New Type of Papillomavirus Associated with Cancer of the Uterine Cervix			
JOURNAL	Virology	159, 187-190 (1991)		
MEDLINE	87265470			
REFERENCE	2	(bases 1 to 7851)		
AUTHORS	Marich,J.E., Pontsler,A.V., Rice,S.M., McGraw,K.A. and Dubensky,T.W.			
TITLE	The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35			
JOURNAL	Virology	186 (2), 770-776 (1992)		
PUBLISHED	1310198			
COMMENT	Original source text: Human papillomavirus type 35 cervical carcinoma DNA.			
FEATURES	Location/Qualifiers			
source	1..7851 /organism="Human papillomavirus type 35" /proviral /mol_type="genomic DNA" /isolation_source="cervical carcinoma" /db_xref="taxon:10587" join(7092..7851,1..109) /standard_name="LCR" /function="regulatory region" 17..22 /bound_moiety="Sp-1" complement(18..26) 24..35 /notes="putative" /bound_moiety="E2" /function="gene transcription" 39..50 /notes="putative" /bound_moiety="E2" /function="gene transcription" 54..59 /notes="putative" 110..559 /gene="E6" 110..559 /gene="E6" /codon_start=1 /product="transforming protein" /protein_id="AAA46966.1" /db_xref="GI:333051"			
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gene	110..559 /gene="E6"			
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RPTRLGLYKGTQGVVDPAFMTSPAKLITYDNPAYEGLNPDITLQFEHEDI SLAP
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ORIGIN
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Best Local Similarity 93.1%; Pred. No. 0.086;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCGTCAGAGGTTACCATAGGCACTAGG 29
Db 6487 GCATCGAGGTTACCATAGGCACTAGG 6459
RESULT 3
HPV30/c HPV30 7852 bp DNA linear VPL 18-APR-2005
LOCUS Human papillomavirus type 30 genomic DNA.
DEFINITION X74474
ACCESSION
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VERSION
KEYWORDS
SOURCE
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TITLE
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HGNKYIYDFDEAVKYGKGTWVHMGNESIYCPDSVSTLRNSVSPETVVEYNT  
YNTQPTTSTVPVGEAASARPGRKPRTPEDSDTTRQSAARESHANRVNTNTN  
NRQCLGATTCYNTVDGGYKTPPVHLKGEPNRLKCLRYRCQKHFLFVNISSYHWT  
NTHTEYSYITVYKDETQRANFLNVVVKIPPSIKIVMGHMTGVDM"

gene 4280. .5671

CDS /gene="L2"

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/db\_xref="GI:396979"

/db\_xref="GOA:P36756"

/db\_xref="InterPro:IPR000784"

/translation="MVHARRKRASATQLYQTCQAGTCPSDVINKIEHTTLADKI  
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IVTLVPESSVWVAGASFPNPTGTAGPEVTSSTTPAVLDITPTGSHVVSSTHTNP  
SVFEPVIEVPQTGEVSGHILVSTPTSGVHSYEEIPMQTFVHVGTEPISSTIPDGL  
RRIAAPRLYQAPQVQVVDPTLTKPETLIIVDNPVEDADTTLTFSPGVAPDPDF  
LDIVLHRAFPATRRGVFRSLGKATWTRSGQIGARVHYVDVSPIAHTEIEM  
QPLLANNPFDGLYDIYANLDEAPVSSHLSIATSRPLTNTVPLSFSSQTTNVTIPL  
KQWDPVPIYSGDPIVLPTGPTTWPYAPQAPEDTHDVIHGTSTFALWPVYFLRRRRK  
HVPYFLADGGVAA"

gene 5631. .7157

CDS /gene="L1"

/gene="L1"

/codon\_start=1

/product="late protein"

/protein\_id="CAA52548.1"

/db\_xref="GI:396980"

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/db\_xref="InterPro:IPR002210"

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GSRLLAVGHYYSISKAGNSKTDVPKSAFQVRVRLPDNPKFGLPDTNVPFPEQ  
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TOLICITGTPAGEHWAGKTACRAPPACQDCPPLVNSPIQDGMVDIGFAMDFFK  
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QVPTVVDVTRNTNMTISATTOTLSTYNSQIKQYVRHVEEYELQVFVOLFCKISAE  
TWAYLMTNMLLEGWNLIGLSPATSLEDKRYVKSALITCOKQPPAERKDLPLAKY  
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ORIGIN

Query Match 89.0%; Score 25.8; DB 13; Length 7852;  
Best Local Similarity 93.1%; Pred. No. 0.086; 2; Indels 0; Gaps 0;  
Matches 27; Conservative 0; Mismatches 2;

QY 1 GCCTCAGAGGTATACCATAGACCACTAGG 29

DB 6562 GCCTCAGAGGTATACCATAGACCACTAGG 6534

RESULT 4

HPV35H/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .7879

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/mol\_type="genomic DNA"

/db\_xref="taxon:31551"

/clone="insert in BamHI site of pBR322"

110. .559

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/db\_xref="GOA:P27228"

/db\_xref="InterPro:IPR001334"

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562. .861

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562. .861

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/db\_xref="InterPro:IPR000148"

/db\_xref="UniProt/Swiss-Prot:P27230"

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868. .2781

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868. .2781

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/db\_xref="GI:397000"

/db\_xref="GOA:P27220"

/db\_xref="InterPro:IPR001177"

/db\_xref="UniProt/Swiss-Prot:P27220"

HPV35H 7879 bp DNA linear VRL 18-APR-2005  
Human papillomavirus type 35H genomic DNA.

X74477 GI:396997  
E1 gene; E2 gene; E4 gene; E6 gene; E7 gene; early protein; L1  
gene; L2 gene; late protein.

Human papillomavirus type 35H  
Human papillomavirus type 35H

Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
Alphapapillomavirus.

1 (bases 1 to 7879)  
Delius,H. and Hofmann,B.

Primer-directed sequencing of human papillomavirus types  
Curr. Top. Microbiol. Immunol. 186, 13-31 (1994)

8205838  
2 (bases 1 to 7879)  
Delius,H.

Direct Submission  
Submitted (06-AUG-1993) H. Delius, Deutsches  
Krebsforschungszentrum, Abteilung ATV, Im Neuenheimer Feld 506, W

6900 Heidelberg, FRG  
Location/Qualifiers

1. .7879  
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/mol\_type="genomic DNA"

/db\_xref="taxon:31551"

/clone="insert in BamHI site of pBR322"

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868. .2781  
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GDSITSSSDERHDETPTRDIIQILKCSNANAAMLAKFKELFGISTELLIRPFKSKST



CTDWCVAARFAGIAPSAESLKTLLIKYCYLIYHICQLSCSGWVILALLRPFCKAKNRTTI  
EXLKLCLISASMLIOPKLRSTPAALYKFAETNSINSEVDGTPSWIQRTVLQH  
SFNDALFOLSEWQAYDNDIFDDSDIAKYAQLAETNSACAFILKSNSQAKIVKQCA  
TMCRYKRAEKREMTSOWIKERCEKVDGDDWRDVRFLRYQQVDVFAFLSALKNFL  
HGVPKNGCILIYAGPNTGSLFCMSLMHPFLOGAIISYVNSKSHFWLQPLADAKIAMLD  
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gene

2714. .52717

CDS

2714. .52717

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gene

4211. .5620

CDS

4211. .5620

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RPTTLGLYSQTKQKVVDPAFTSPAKLITDYNPAVEGLNPDTLQFEHEDSLAP  
DPFDNIALHPALTSRGTIRSRVGNKTMTRSKAIGARHYHQDLSSTEDI  
ELQPHVPSLPHPTVTSVDSGMFDIYAPIDTEEDLIIFASSNNITLYTNSATVP  
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gene

5601. .7109

CDS

5601. .7109

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CRPPIGHWGKTPCNAVQKAGECPLELLNTVLQDGMVDVTFGAMDFTTLQANS  
DVPLDICSICKYDPLKMSVSEPGDMLFFYLRRQMFVRHLFNRAGTVGETVADLY  
IKGTITSYPTSPSTPGSMVTSDAQIFNKPYLWRAQGHNGICMSNQLFVTVDT  
TRSTNMSVCSAVSSSDSYTKNDNFKEYLRHGEYDLOFIOLCKITLTALVMTYIHS  
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EKFSAADLQDFLGRKFLLOGLKARPNFLGRKRAAPASTSKSSSTKRRKVS"

## ORIGIN

Query Match 89.0%; Score 25.8; DB 13; Length 7879;  
Best Local Similarity 93.1%; Pred. No. 0.086;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29

Db 6505 GCATCGGAGGTTACCATAGAGCCACTAGG 6477  
|||||

RESULT 5

HPU37488/c

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

HPU37488 7759 bp DNA linear VRL 06-DEC-1999  
Human papillomavirus type 54, complete genome.  
U37488  
U37488.1 GI:1017782

Human papillomavirus - 54  
Human papillomavirus - 54  
Alphapapillomavirus.  
1 (bases 1 to 7759)  
Delius H.  
Unpublished

2 (bases 1 to 7759)  
Farmer A.D.F.  
Direct Submission

Submitted (03-OCT-1995) Andrew Farmer, Los Alamos National  
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los  
Alamos, NM 87501 USA

HPV-54 was first isolated from a patient with condyloma acuminata.

FEATURES  
source

1..7759  
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/mol\_type="genomic DNA"  
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gene

CDS

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IRCLWCKPLCNVEKQHRVDYNNRHFCHVGRGKRCCLHCWRP"  
536..823  
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gene

CDS

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gene

CDS

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RHVTRAKOMTMSQWIKHRCDLVEEGENKEI VRFLRYOHVDIFSFIALKQFLQGI  
PKNICLLYGPDPKSNFMSLISFLGGVVLVSYNSSSHFWLPLADAKIAMLDDAT  
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2671..3774  
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2671..3774  
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gene

CDS

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CDS 3134..3538  
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EIELPHLSANTNNGLYSDIYADTFADTGFSSSTVSHSVOTLAQTSIP  
SOYGNTPVLTASSPYTPTIFRPSSTGTPFPVAPRIPPTPIAVNGGDFYLPSPY  
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SNLSSIIYAATPSSSMWTSYQIFNKPFWLQRAQONQICWGNQVFLTVVDVTRST  
NLTLCAATQDSFNNSDPREYIRHVEEYDLOFIFQCLCTITLADVMAYIHGMNPTIL  
EDWNTGITPATSSLEDYTFVQSAIAQCKNNAFAKEDPYSKFNFTVLDKERFS  
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ORIGIN

Query Match 84.1%; Score 24.4; DB 13; Length 7759;  
Best Local Similarity 96.2%; Pred. No. 0.44;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 TCAGAGGTTTACCATAGCCACTAGG 29  
DB 6503 TCAGATGTTACCATAGCCACTAGG 6478

RESULT 6  
AF293961/c 7904 bp DNA linear VRL 02-APR-2001  
LOCUS Human papillomavirus type 82 subtype IS39/AE2, complete genome.  
DEFINITION

AF293961 AF293961.1 GI:13507120  
VERSION Human papillomavirus type 82  
KEYWORDS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
SOURCE Alhappapillomavirus.  
ORGANISM 1 (bases 1 to 7904)  
REFERENCE 1 (bases 1 to 7904)  
AUTHORS Terai,M. and Burk,R.D.  
TITLE Cervical HPV8 in Evolution; Genomic Sequence of IS39/AE2, a Subtype of Oncogenic HPV 82 (W13B)  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 7904)  
AUTHORS Burk,R.D. and Terai,M.  
TITLE Direct Submission  
JOURNAL Submitted (07-AUG-2000) Microbiology & Immunology, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10461, USA  
FEATURES  
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KYKDCGNTTHRYKRAQKSLTMSAWIRYRCDKVADGGNREIAKFLRYOGINFWYFI  
QTKFLFKGTGPKHNCIVIQGPNQTSQFAMSLRPLQGCIIISYNSGSHFWLQPLED  
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PDVHKYVKGFTIEAKYCAQOQEVVMCGNVITCEYVSSITCRDPLPSTVTVQHSNT  
PTNTYVTSVGTKEAQAQPOQRQRITPDSSTVTPLSVDTCDHOIHGCTGSAHTGH  
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3788..4036  
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/db\_xref="GI:13507126"  
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4068..5489  
/gene="L2"  
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/product="putative minor capsid protein L2"  
/protein\_id="AAK28455.1"  
/db\_xref="GI:13507127"

gene

CDS

/translation="WVAARRRKRASVTQLYSTCKAAGTCPADVIPKVGTTLADKI  
LWMSGLGIFLAGLIGTSGTGRTGYIPLGGGRPGVVDIAPAPPIIIEPVAPTEP  
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PLYIPPTAPQSEVSGHIFTPTSGTHGYEIPMEVFASNVSTGEOPISSTPTP  
GVRLAARPLYSKATQVKNVNPDIISRPSSFTPDNPAFIDASLSPGETTVAPD  
PFLDIILHRPALTSRGTVRFSLGQKATIRSGKQIGARVHYHIDENITITPE  
LEMQLPSPSTNNYSYDIADLDEAETGFIQHTTTPMLRSSYSLSTHOLPSLSSVS  
SSYANVTIPFTTTHVPTITGPDVLTPTSPVWPFIPHTSIDTQHAIVIQGGDYLLP  
YTLRKRKRIPFFADGFAY"  
5470..5981  
/gene="L1"  
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/codon\_start=1  
/product="putative major capsid protein L1"  
/protein\_id="AAK28456.1"  
/db\_xref="GI:13507128"

gene

CDS

/translation="WALWRKNDKVLPPAPVSRIVNTEEYITRTGIYYAGSSRLIT  
LGHPYFPLSTRAEIKFSAFYQVRFVQVLPDKNFGLPDNLFNPDRLVWGVC  
GVEVGRQPLGVLGSLFENKVDITENSANGVNOQDVDRNISVDNKQTLCTIGC  
APPIGEHWATGTCNVVPOGDCPLBLVSTIIEGDMIDTGCAMDFAILOATKSD  
VPLDIAQVCKYDPDKWSADTVGNMFEHLRQEI FARHYNRAGVVGDALPDKAYI  
KGTGGRDPIGSYIYSATPSGSMVTSDSQIFNKPYLHRAQGNHNGICWNQOLFICV  
DTTSTNITATPASPVAQFTPTNFQYIRHGBEYELQIFQLCKITLTTEVNAYL  
HTMDSITILEQWNGFTLPPSASLEDAYRFVKNATSCQDPSPPQAKODPLAKYFVTV  
DLKERFSLDLQALGRKFLQIGAQKARPKLKPAPSSSSSSSKRKRVKK"

ORIGIN

Query Match 84.1%; Score 24.4; DB 13; Length 7904;  
Best Local Similarity 96.2%; Pred. No. 0.44;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCAGAGGTTACCATAGCCACTAG 29.

Db 6377 TCAGAGGTTACCATAGCCACTTG 6352

RESULT 7  
AY098925/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..624

/organism="Human papillomavirus type 16"

/virus="Papillomaviridae"

Alphapapillomavirus

1 (bases 1 to 624)

Cruz, M.R., Cerqueira, D.M., Camara, G.N.L., Silva, E.O.,

Carvalho, L.G.S. and Martins, C.R.F.

Human papillomavirus type 16 variants in Central Brazil

2 (bases 1 to 624)

Cruz, M.R. and Martins, C.R.F.

Direct Submission

Submitted (23-APR-2002) Cellular Biology, UnB, Campus UnB,

Brasilia, DF 70.910-900, Brazil

Location/Qualifiers

1..624

/organism="Human papillomavirus type 16"

/virus="Papillomaviridae"

Alphapapillomavirus

1 (bases 1 to 624)

Cruz, M.R., Cerqueira, D.M., Camara, G.N.L., Silva, E.O.,

Carvalho, L.G.S. and Martins, C.R.F.

Human papillomavirus type 16 variants in Central Brazil

2 (bases 1 to 624)

Cruz, M.R. and Martins, C.R.F.

Direct Submission

1..624

/organism="Human papillomavirus type 16"

/virus="Papillomaviridae"

Alphapapillomavirus

1 (bases 1 to 624)

Cruz, M.R., Cerqueira, D.M., Camara, G.N.L., Silva, E.O.,

Carvalho, L.G.S. and Martins, C.R.F.

Human papillomavirus type 16 variants in Central Brazil

2 (bases 1 to 624)

Cruz, M.R. and Martins, C.R.F.

Direct Submission

1..624

/organism="Human papillomavirus type 16"

/virus="Papillomaviridae"

Alphapapillomavirus

1 (bases 1 to 624)

Cruz, M.R., Cerqueira, D.M., Camara, G.N.L., Silva, E.O.,

Carvalho, L.G.S. and Martins, C.R.F.

Human papillomavirus type 16 variants in Central Brazil

2 (bases 1 to 624)

Cruz, M.R. and Martins, C.R.F.

Direct Submission

1..624

/organism="Human papillomavirus type 16"

/virus="Papillomaviridae"

Alphapapillomavirus

1 (bases 1 to 624)

Cruz, M.R., Cerqueira, D.M., Camara, G.N.L., Silva, E.O.,

Carvalho, L.G.S. and Martins, C.R.F.

Human papillomavirus type 16 variants in Central Brazil

2 (bases 1 to 624)

Cruz, M.R. and Martins, C.R.F.

Direct Submission

```

YKNTNFKVLRHGEYDQLQFIQOLCKITLTADWMTYIHSMNSTILEDWNFGIQPPGGL
TLEDYRFVTQTQAICOKHTPPAPKKEDPLUKYTFWEVNLIKERFSADLDQFLGRKEFL
QAG"

ORIGIN
Query Match      83.4%; Score 24.2; DB 13; Length 667;
Best Local Similarity 89.7%; Pred. No. 0.64;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy    1 GCCTCAGAGGTATACCATAGAGCCACTAGG 29
      ||| ||||| ||||| ||||| ||||| |||||
Db    157 GCATCAGAGTTAACCATAGACCCTAGG 129

RESULT 10
DQ003067/c
LOCUS              799 bp      DNA          linear       VRL 15-AUG-2005
DEFINITION Human papillomavirus type 16 L1 gene, partial cds.
ACCESSION DQ003067
VERSION     DQ003067.1 GI:66866320
KEYWORDS   .
SOURCE     Human papillomavirus type 16
ORGANISM   Human papillomavirus type 16
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE  1 (bases 1 to 799)
AUTHORS   Wu,X., Ren,J., Ran,D. and Ma,R.Z.
TITLE     Detection of HPV types in cervical brush samples of clinical
           patients in Beijing and other Northern China cities
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 799)
AUTHORS   Wu,X., Ren,J. and Ma,R.Z.
TITLE     Direct Submission
JOURNAL   Submitted (08-APR-2005) Institute of Genetics and Developmental
           Biology, Chinese Academy of Sciences, A5 Datun Raod, Chaoyang
           District, Beijing 100101, China
FEATURES   Location/Qualifiers
             1..799
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               /db_xref="taxon:333760"
               /country="China"
               <1..>799
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                 /gb_xref="GI:66866321"
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PGDCPLEINTVIQGDWDFGAMDFTTLQANKSEVPDLICTSI CKYPDYIKMVS
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SWTSDAQIFNKPYLMQRAQHNGICWGKQLFVTVDTRSTNMSLCAAISTSETTY
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CDS

ORIGIN
Query Match      83.4%; Score 24.2; DB 13; Length 799;
Best Local Similarity 89.7%; Pred. No. 0.63;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy    1 GCCTCAGAGGTATACCATAGAGCCACTAGG 29
      ||| ||||| ||||| ||||| ||||| |||||
Db    501 GCATCAGAGTTAACCATAGACCCTAGG 473

RESULT 11
AF512011/c
LOCUS              1257 bp      DNA          linear       VRL 02-JUL-2002
DEFINITION Human papillomavirus type 16 L1 protein (L1) gene, partial cds.
ACCESSION AF512011
VERSION     AF512011.1 GI:21667875
KEYWORDS   .
SOURCE     Human papillomavirus type 16

```

ORGANISM Human papillomavirus type 16  
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
Alphapapillomavirus.  
REFERENCE 1 (bases 1 to 1257)  
AUTHORS Zhang, J. and Chen, R.  
TITLE Cloning and sequence analysis of Human papillomavirus type 16 L1 gene in China  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1257)  
AUTHORS Zhang, J. and Chen, R.  
TITLE Direct Submission  
JOURNAL Submitted (15-MAY-2002) Fourth Military Medical University,  
Institute of Gene Diagnosis, Changlie West Road 17, Xian, Shaanxi  
710032, China

FEATURES  
source Location/Qualifiers  
1..1257  
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    /country="China"  
gene 1..>1257  
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CDS 1..>1257  
    /gene="L1"  
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        /product="L1 protein"  
        /protein\_id="AAW74159.1"  
        /db\_xref="GI:21667876"  
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SKVSTDEVVARTNIYYHACTSRLLAVGHYPPIKNNKKILVPKVGSLQYRVFTRHL  
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ORIGIN  
Query Match 83.4%; Score 24.2; DB 13; Length 1257;  
Best Local Similarity 89.7%; Pred. No. 0.62;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GCCTCAGAGTTACCATAGCCACTAGG 29  
|| ||||||| ||||||| |||||||  
Db 986 GCATCAGAGTAACCATAGAACCCTAGG 958  
  
RESULT 12  
AX770809/c  
LOCUS AX770809 1452 bp DNA linear PAT 02-JUL-2003  
DEFINITION Sequence 2 from Patent WO03018623.  
ACCESSION AX770809  
VERSION AX770809.1 GI:32437978  
KEYWORDS  
SOURCE Human papillomavirus  
Human papillomavirus  
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
unclassified Papillomaviridae.  
1 Varsani,A.D., Rybicki,E.P. and Williamson,A.L.  
Pharmaceutical compositions, and a method of preparing and  
isolating said pharmaceutical compositions, and use of said  
pharmaceutical compositions for prophylactic treatment of lesions  
and carcinomas  
Patent: WO 03018623-A 2 06-MAR-2003;  
University of Cape Town (ZA)  
LOCATION/Qualifiers  
1..1452  
    /organism="Human papillomavirus"  
    /mol\_type="unassigned DNA"  
    /db\_xref="taxon:10566"

ORIGIN

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RESULT 15
HPU34165/c
LOCUS
DEFINITION
  Human papillomavirus type 16, isolate NM 4094, late major capsid
  protein L1 (L1) gene, partial cds.
ACCESSION
  U34165
VERSION
  U34165.1
KEYWORDS
  U34165.1 GI:1098837
ORGANISM
  Human papillomavirus
  Human papillomavirus
  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
  unclassified Papillomaviridae.
REFERENCE
  1 (bases 1 to 1484)
  Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
  and Jenison,S.A.
  Human papillomavirus type 16 variant lineages in United States
  populations characterized by nucleotide sequence analysis of the
  E6, L2, and L1 coding segments
  J. Virol. 69 (12), 7743-7753 (1995)
7494284
  2 (bases 1 to 1484)
  Farmer,A.D.
  Direct Submission
  Submitted (17-AUG-1995) Andrew D. Farmer, Los Alamos National
  Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
  Alamos, NM 87501, USA
  Location/Qualifiers
    1. .1484
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      /mol_type="genomic DNA"
      /isolate="NM 4094"
      /db_xref="taxon:10566"
      /notes="collected by cervical swab at the University of New
      Mexico, New Mexico, United States."
    1. .1484
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      /product="late major capsid protein L1"
      /protein_id="AAA91712.1"
      /db_xref="GI:1098838"
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      GKSPCNVAVTPGDCPPLLEINTVIQDGMVDITGFGAMDFTTLQANKSEVPLDICTS
      ICKYPDYIKWVSEPYGDSLFFYLRRQMFVRLFNAGAVGNVPDDLVIKGGSGSTAN
      LASSNYPPTPSGSMVTSDAQIENKPYMLOAOGHNGICWGNQLFVTVVDTTRSTNMS
      LCAISTSEPTYNTPKEYLRHGEYDLQFIQLCKITLTADVMSYIHSNMSTILED
      WNFGLQPPPGTLEDTYRFVTSQAIACQKHTPPAKDEPLKRYTFWEVNLKKEKFSADL
      DQPLGRKFLQAGFKAKPKFTLGRKATPTTSTSTTAKRKR"
ORIGIN
  Query Match 83.4%; Score 24.2; DB 13; Length 1484;
  Best Local Similarity 89.7%; Pred. No. 0.61;
  Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
  QY 1 GCCTCAGAGGTTACCATAGAGCCACTAGG 29
  ||| ||||| ||||| ||||| |||||
  Db 884 GCATCAGAGGTACCATAGAGCCACTAGG 856

Search completed: March 5, 2006, 22:23:15
Job time : 908 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:08:34 ; Search time 271.5 Seconds  
(without alignments)  
711.882 Million cell updates/sec

Title: US-10-720-424B-1

Perfect score: 29  
Sequence: 1 gatgtatattgtatgacagattg 29

Scoring table: OLIGO-NUC  
Gapop-60.0, Gapext 60.0

Searched: 4996997 seqs, 332346308 residues

Word-size: 1

Total number of hits satisfying chosen parameters: 5288170

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001as.\*  
5: Geneseq2001bs.\*  
6: Geneseq2002as.\*  
7: Geneseq2002bs.\*  
8: Geneseq2003as.\*  
9: Geneseq2003bs.\*  
10: Geneseq2003cs.\*  
11: Geneseq2003ds.\*  
12: Geneseq2004as.\*  
13: Geneseq2004bs.\*  
14: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	29	12	Adq27974 Human pap
2	24	48.3	25	9	Acil16395 Human mic
3	14	48.3	38	2	AaQ23183 HPV probe
4	14	48.3	38	2	AaQ29878 Human pap
5	13	44.8	13	5	Abf76716 Oligonuc
6	13	44.8	13	5	Abf76717 Oligonuc
7	13	44.8	17	6	Abk56011 Human CLC
8	13	44.8	17	6	Abk57740 Human CLC
9	13	44.8	17	6	Abk57423 Human CLC
10	13	44.8	21	2	AaQ61872 DNA cap
11	13	44.8	21	2	AaV07712 HPV-18 pr
12	13	44.8	21	12	AdO78152 Human CLC
13	13	44.8	21	13	AdU26858 Knock-dow
14	13	44.8	24	12	AdQ27975 Human pap
15	13	44.8	41	6	Abn84687 HIV-1 amp
16	13	44.8	41	6	Abz46492 Human ALD
17	13	44.8	41	6	Abz49020 Human ALD
18	13	44.8	42	12	AdG00344 Nicotiana
19	13	44.8	46	10	AdH94574 Gene prom

20	13	44.8	61	2	AAT29759	Aat29759 D10 eCTCR
21	12	41.4	17	6	ABK57201	Abk57201 Human CLC
22	12	41.4	17	6	ABK56012	Abk56012 Human CLC
23	12	41.4	18	2	AAQ39483	AaQ39483 PCR Prime
24	12	41.4	18	6	ABK40943	Abk40943 Human obe
25	12	41.4	18	13	ADS90978	AdS90978 Oligonuc
26	12	41.4	18	14	AEA80760	Aea80760 Human tum
27	12	41.4	20	2	AAx94223	Aax94223 PCR prime
28	12	41.4	20	4	AAS42900	Aas42900 Human G P
29	12	41.4	20	12	ADP68078	AdP68078 Human jag
30	12	41.4	20	12	ADP68043	AdP68043 Human jag
31	12	41.4	21	2	AAV32488	Aav32488 Human ret
32	12	41.4	21	3	AAZ55850	Aaz55850 Human ret
33	12	41.4	23	12	ADN35455	Adn35455 Human NSC
34	12	41.4	25	9	ACI49246	AcI49246 Human mic
35	12	41.4	25	9	ACK15509	Ack15509 Human mic
36	12	41.4	25	9	ACI16394	AcI16394 Human mic
37	12	41.4	25	9	ACK28706	Ack28706 Human mic
38	12	41.4	29	10	ADE37863	AdE37863 CpG islan
39	12	41.4	29	14	ADW01878	AdW01878 DNA probe
40	12	41.4	31	6	ABK86296	Abk86296 Human TGR
41	12	41.4	41	6	ABZ43753	Abz43753 Human alc
42	12	41.4	41	6	ABZ49321	Abz49321 Human alc
43	12	41.4	47	3	AAZ67316	Aaz67316 Human map
44	12	41.4	48	4	AAS42897	Aas42897 Human G P
45	12	41.4	50	4	AAI77901	Aai77901 Human sil

#### ALIGNMENTS

##### RESULT 1

ADQ27974  
ID ADQ27974 standard; DNA; 29 BP.  
XX  
AC ADQ27974;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human papillomavirus genotype detection PCR primer #4.  
XX  
KW ss; primer; detection; diagnosis; amplification;  
Human Papillomavirus genotype; cervical-neoplasia;  
oncogenic high-risk group.  
KW  
XX  
OS Human papillomavirus.  
XX  
PN WO2004050917-A1.  
XX  
PD 17-JUN-2004.  
XX  
PF 28-NOV-2003; 2003WO-KR002608.  
XX  
PR 29-NOV-2002; 2002KR-00075370.  
PR 31-JUL-2003; 2003KR-00053147.  
(ALBI-) ALBIOMED CO LTD.  
PI Lee S, Kim Y, Yu K, Kim S, Cha K, Ko J;  
XX  
DR WPI; 2004-450746/42.  
XX  
PT New general primer or primer pair, useful for amplifying and detecting,  
or for use in a nucleic acid amplification process for amplifying Human  
Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV  
genotypes.  
PS Claim 1; SEQ ID NO 4; 71pp; English.  
XX  
CC The invention relates to a general primer or primer pair for amplifying  
and detecting or for use in a nucleic acid amplification process for  
amplifying Human Papillomavirus (HPV) genotypes. The general primers are  
useful for amplifying cervical-neoplasia related HPV genotypes including

CC oncogenic high-risk groups and low-risk groups. The general primers are  
 CC useful for producing amplifying products to DNA of scores of diverse  
 CC oncogenic HPV types and thus detecting the oncogenic HPV types in a  
 CC sample but also to select cervical carcinoma and its pre-stage lesions at  
 CC early stage by improving sensitivity according to HPV types. This  
 CC sequence corresponds to PCR primer used in the invention.

XX Sequence 29 BP; 8 A; 1 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 29; DB 12; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGGTATGCTAGATACAGGATTGG 29  
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 DB 1 GATGGTATGCTAGATACAGGATTGG 29

RESULT 2

AC116395/c  
 ID AC116395 standard; DNA; 25 BP.

XX AC

XX AC116395;

XX DT 13-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 16386.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; biallelic marker; polymorphism; human;  
 KW cross-species comparison.

XX OS Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mitmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 16386; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying biallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been

CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
 XX  
 SQ Sequence 25 BP; 7 A; 7 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 48.3%; Score 14; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGGTAGATACAGG 23  
 |||||  
 DB 25 ATGGTAGATACAGG 12

RESULT 3

AAQ23183  
 ID AAQ23183 standard; DNA; 38 BP.

XX AC

XX AC AAQ23183;

XX DT 06-AUG-1992 (first entry)

XX DE HPV probe 36.

XX KW Human papilloma virus; LCR; ligase chain reaction; ss.  
 XX Synthetic.  
 XX EP477972-A.

XX PD 01-APR-1992.

XX PF 27-SEP-1991; 91EP-00116561.

XX PR 28-SEP-1990; 90US-00589948.

XX PR 28-SEP-1990; 90US-00590105.

XX PR 28-SEP-1990; 90US-00590253.

XX PA (ABBO ) ABBOTT LAB.

XX PI Joseph JL, Bouma SR, Marshall RL, Laffler TG;

XX WPI; 1992-106365/14.

XX Compens. for amplifying DNA of human papilloma virus by LCR and PCR - and  
 PT consensus and type specific oligo-nucleotide(s), for diagnosis of HPV-  
 PT esp. types 6,11,16,18 33 and 61.  
 XX Claim 18 + Example 5; Page 69 + 11-13; 76pp; English.

XX Probe 36 maps to HPV types 6 (6365-6402), 11 (6350-6387), 16 (6225-6262),  
 CC 18 (6201-6238) and 33 (6182-6219). Sequences were selected according to  
 CC an unique algorithm developed to choose consensus sequences. The  
 CC sequences represented in AAQ23167-88 are consensus sequences selected so  
 CC each should hybridise with each of human HPV types 6, 11, 16, 18 and 33.  
 CC The sequences represented in AAQ23095-189 and AAQ25590 allow the  
 CC detection of small ants. of HPV DNA, e.g. from cervical lesion samples,  
 CC using PCR or LCR amplification procedures. The use of nucleic acids  
 CC allows greater discrimination among viral subtypes than antibodies, and  
 CC the use of DNA-based tests increases both the sensitivity and the  
 CC specificity of prior-art antibody based tests. The oligonucleotides can  
 CC be used either to detect specific sequences of specific HPV types, or  
 CC consensus regions with homology among different types

XX Sequence 38 BP; 8 A; 3 C; 14 G; 13 T; 0 U; 0 Other;

Query Match 48.3%; Score 14; DB 2; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGGTATGATGGT 14



```
Db      1  GATGGTGATGCT 14
|||||
RESULT 4
AAT29878
ID  AAT29878 standard; DNA; 38 BP.
XX
AC  AAT29878;
XX
DT  25-MAR-2003 (revised)
DT  19-JUL-1996 (first entry)
XX
DE  Human papillomavirus detection probe 36.
XX
KW  primer; probe; human papillomavirus; PCR; amplification; LCR; ligation;
KW  fluorescein; biotin; ss.
XX
OS  Synthetic.
XX
FN  US5484699-A.
XX
PD  16-JAN-1996.
XX
PF  30-SEP-1994; 94US-00316293.
XX
PR  28-SEP-1990; 90US-00589948.
PR  28-SEP-1990; 90US-00590105.
PR  28-SEP-1990; 90US-00590253.
PR  22-OCT-1992; 92US-00965665.
XX
PA  (ABBO ) ABBOTT LAB.
XX
PI  Marshall RL, Bouma SR, Latfler TG, Joseph JL;
XX
WPI; 1996-087060/09.
XX
New human papilloma virus type-specific oligo:nucleotide(s) - used for
the detection of and determination of the type of HPV in test samples.
XX
Example 5; Col 13-14; 37pp; English.
XX
The sequences AAT29826-729921 represent primers and probes derived from
human papillomavirus genomic sequences and are used to detect the presence
of human papillomavirus types 6, 11, 16, 18, 31 and 33 in samples. The
detection is either by PCR or ICR. Alternatively the sequences can be
labelled with fluorescein or biotin and used as probes. (Updated on 25-
MAR-2003 to correct PF field.)
XX
SQ  Sequence 38 BP; 8 A; 3 C; 14 G; 13 T; 0 U; 0 Other;
Query Match 48.3%; Score 14; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  1  GATGGTGATGCT 14
Db      1  GATGGTGATGCT 14
|||||
RESULT 5
ABF76716
ID  ABF76716 standard; DNA; 13 BP.
XX
AC  ABF76716;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide SEQ ID NO 176713 for detecting SNP TSC0043853.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX  Homo sapiens.
XX  WO200177384-A2.
XX  18-OCT-2001.
XX  06-APR-2001; 2001WO-IB000713.
XX  07-APR-2000; 2000DE-01019173.
XX  (EPIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
Claim 1; SEQ ID NO 176713; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
-ABC99899, ABF0010-ABF99899, ABH0010-ABH99899 and AB10010-AB182073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 44.8%; Score 13; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  4  GGTGATGCTAG 16
Db      1  GGTGATGCTAG 13
|||||
RESULT 6
ABF76717/c
ID  ABF76717 standard; DNA; 13 BP.
XX
AC  ABF76717;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide SEQ ID NO 176714 for detecting SNP TSC0043853.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX  Homo sapiens.
XX  WO200177384-A2.
XX  18-OCT-2001.
XX  06-APR-2001; 2001WO-IB000713.
XX  07-APR-2000; 2000DE-01019173.
XX  (EPIG-) EPIGENOMICS AG.
XX
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PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 176714; 29pp + Sequence listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABJ00010-ABJ82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 44.8%; Score 13; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GGTGATATGGTAG 16  
DB 13 GGTGATATGGTAG 1  
RESULT 7  
ABK56011  
ID ABK56011 standard; RNA; 17 BP.  
XX  
XX ABK56011;  
AC  
XX 02-JUL-2002 (first entry)  
DT  
XX  
DE Human CLCA1 gene enzymatic nucleic acid #382.  
XX  
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW acetylcysteine.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200211674-A2.  
PN  
XX 14-FEB-2002.  
PD  
XX  
XX 09-AUG-2001; 2001WO-US024970.  
PF  
XX  
XX 09-AUG-2000; 2000US-0224383P.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (SYNT) SYNTAX USA LLC.  
PA (THOM/) THOMPSON J.  
XX  
XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grupe A;  
XX  
XX WPI; 2002-217145/27.  
DR  
XX  
XX Enzymatic polynucleotide that down regulates expression of chloride  
PT channel calcium activated gene, useful for treating Chronic obstructive  
PT pulmonary disease (COPD), Chronic bronchitis and asthma.  
XX

PS Claim 4; Page 59; 152pp; English.  
XX  
XX The invention relates to enzymatic nucleic acid molecules that down  
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic  
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of CLCA1 in a cell or  
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of CLCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of CLCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention  
XX  
XX Sequence 17 BP; 6 A; 2 C; 5 G; 0 T; 4 U; 0 Other;  
SQ  
Query Match 44.8%; Score 13; DB 6; Length 17;  
Best Local Similarity 76.9%; Pred. No. 1.3e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 10 ATGGTAGATACAG 22  
DB 4 AUGGUAGUACAG 16  
RESULT 8  
ABK57740  
ID ABK57740 standard; RNA; 17 BP.  
XX  
XX ABK57740;  
AC  
XX 02-JUL-2002 (first entry)  
DT  
XX  
DE Human CLCA1 gene enzymatic nucleic acid #2111.  
XX  
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW acetylcysteine.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200211674-A2.  
PN  
XX 14-FEB-2002.  
PD  
XX  
XX 09-AUG-2001; 2001WO-US024970.  
PF  
XX  
XX 09-AUG-2000; 2000US-0224383P.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (SYNT) SYNTAX USA LLC.  
PA (THOM/) THOMPSON J.  
XX  
XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grupe A;  
XX  
XX WPI; 2002-217145/27.  
DR  
XX  
XX Enzymatic polynucleotide that down regulates expression of chloride  
PT channel calcium activated gene, useful for treating Chronic obstructive  
PT pulmonary disease (COPD), Chronic bronchitis and asthma.  
XX  
XX Claim 4; Page 134; 152pp; English.  
PS  
XX  
XX The invention relates to enzymatic nucleic acid molecules that down  
CC

CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic  
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of CLCA1 in a cell or  
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of CLCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of CLCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention  
XX  
SQ Sequence 17 BP; 6 A; 1 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 44.8%; Score 13; DB 6; Length 17;  
Best Local Similarity 76.9%; Pred. No. 1.3e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGGTAGATACAG 22  
|:|:|:|:|:|:|  
Db 3 AUGGUAUAUACAG 15

## RESULT 9

ABK57423  
ID ABK57423 standard; RNA; 17 BP.

XX AC ABK57423;

XX 02-JUL-2002 (first entry)

DE Human CLCA1 gene enzymatic nucleic acid #1794.

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW acetylcysteine.

OS Homo sapiens.

XX WO200211674-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US024970.

XX 09-AUG-2000; 2000US-0224383P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTX USA LLC.

PA (THOM/) THOMPSON J.

PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grupe A;

XX WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride  
PT channel calcium activated gene, useful for treating Chronic obstructive  
PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX Claim 4; Page 113; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down  
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic

CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of CLCA1 in a cell or  
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of CLCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of CLCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention  
XX  
SQ Sequence 17 BP; 6 A; 1 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 44.8%; Score 13; DB 6; Length 17;  
Best Local Similarity 76.9%; Pred. No. 1.3e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGGTAGATACAG 22  
|:|:|:|:|:|:|  
Db 2 AUGGUAUAUACAG 14

## RESULT 10

AAQ61872  
ID AAQ61872 standard; DNA; 21 BP.

XX AC AAQ61872;

XX 25-MAR-2003 (revised)

XX 25-OCT-1994 (first entry)

DE DNA capture probe for detection of HPV-18 by sandwich assay.

XX Human papilloma virus; HPV; detection; assay; cervical cancer;  
KW nucleic acid hybridisation; capture probe; sandwich assay; ss.

OS Synthetic.

XX WO9406933-A1.

XX 31-MAR-1994.

XX 21-SEP-1993; 93WO-BE000063.

XX 22-SEP-1992; 92BE-00000827.

XX (LAMB-) LAMBDATTECH SA.

XX Remacle J, Rentier B, Alexandre I, Morris P, Zammatteo N;

XX WPI; 1994-118481/14.

XX New conjugate for bio:luminescent hybridisation or immunoassay -  
PT comprises kinase or dehydrogenase coupled to specific ligand for the  
PT analyte, partic. for detecting human papilloma virus.

XX Example 2B; Page 23; 43pp; French.

XX The capture oligonucleotide AAQ61872 has unique specificity for the HPV-  
CC 18 genome and is complementary to the region around nucleotide 6779 of  
CC HPV-18. The capture probe is immobilised for use in a sandwich  
CC hybridisation assay. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 21 BP; 5 A; 0 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 44.8%; Score 13; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGGTGATATCG 13

Db 9 GATGGTGATATGG 21  
|||||

## RESULT 11

AAV0712  
ID AAV0712 standard; DNA; 21 BP.

XX AC  
XX AAV0712;  
XX DT

XX 25-NOV-1998 (first entry)  
XX DE

XX HPV-18 primer.  
XX XX

XX HPV-18; CMV; cytomegalovirus; detection; quantifying; target nucleotide;  
XX KW capture probe; PCR; primer; ss.

XX OS Synthetic.  
XX OS Human papillomavirus.

XX PN WO9811253-A2.  
XX XX

XX 19-MAR-1998.  
XX PD

XX 09-SEP-1997; 97WO-BE000102.  
XX PF

XX 09-SEP-1996; 96BE-00000755.  
XX PR

XX 20-MAR-1997; 97BE-00000244.  
XX PR

XX (REMA/) REMACLE J.  
XX PA

XX Remacle J, Alexandre I, Zammatteo N, Ernest I;  
XX PI

XX WPI; 1998-207411/18.  
XX DR

XX Sandwich-type nucleic acid hybridisation assay - using long, highly  
XX PT complementary capture probe.

XX Example 1; Page 43; 77pp; French.  
XX PS

XX The invention relates to a method for detecting and/or quantifying a  
XX target nucleotide sequence in a biological sample. It comprises  
XX contacting the sample with an immobilised capture probe and a labelled  
XX detection probe. The capture probe is a single-stranded oligonucleotide  
XX that is complementary to part of the target sequence and is covalently  
XX coupled at one end to a solid support. The detection probe is  
XX complementary to another part of the target sequence. The capture probe  
XX has a length of 50-500 bases, and a portion of the capture probe that  
XX does not hybridise with the target sequence. Use of long, highly  
XX complementary capture probes improves specificity and sensitivity. The  
XX present sequence represents a human papillomavirus (HPV)-18 primer  
XX SQ

Sequence 21 BP; 5 A; 0 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 44.8%; Score 13; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GATGGTGATATGG 13  
Db 9 GATGGTGATATGG 21  
|||||

## RESULT 12

ADO78152  
ID ADO78152 standard; DNA; 21 BP.

XX AC  
XX ADO78152;  
XX XX

XX 26-AUG-2004 (first entry)  
XX DT

XX Human CLCA1 RT-PCR primer #1.  
XX DE

KW ss; reverse transcriptase; RT-PCR; primer; tumour-associated antigen;  
KW TAG; cancer; lung cancer; breast cancer; prostate cancer; colon cancer;  
KW stomach cancer; pancreatic cancer; ear cancer; nose cancer;  
KW throat cancer; kidney cancer; cervical cancer; melanoma; tumour; human;  
KW CLCA1.

XX OS Homo sapiens.

XX PN DE10254601-A1.  
XX PD

XX 03-JUN-2004.  
XX XX

XX 22-NOV-2002; 2002DE-01054601.  
XX PF

XX 22-NOV-2002; 2002DE-01054601.  
XX PR

XX (GANY-) GANYMED PHARM AG.  
XX PA

XX Tuereci O, Sahin U, Koslowski M;  
XX PI

XX WPI; 2004-421820/40.  
XX DR

XX Composition containing inhibitor of expression or activity of specific  
XX PT tumor-associated antigens, useful for treating cancers, also related  
XX PT compositions for diagnosis and monitoring.

XX Example 6; SEQ ID NO 67; 124pp; German.  
XX PS

XX The invention relates to pharmaceutical compositions that comprise an  
XX agent that inhibits the expression or activity of a tumour-associated  
XX antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical  
XX compositions and related compositions, are used for treatment of diseases  
XX associated with (abnormal) expression of TAG, specifically cancer e.g. of  
XX lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney  
XX or cervix, also melanoma. Compositions containing TAG, or related nucleic  
XX acid, antibodies or host cells, are also useful for diagnosis and  
XX monitoring of tumours. The present sequence represents a human CLCA1  
XX reverse transcriptase (RT)-PCR primer.

XX Sequence 21 BP; 8 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 44.8%; Score 13; DB 12; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 10 ATGGTAGATACAG 22  
Db 7 ATGGTAGATACAG 19  
|||||

## RESULT 13

ADU26858/c

ID ADU26858 standard; DNA; 21 BP.

XX AC ADU26858;

XX 27-JAN-2005 (first entry)  
XX DT

XX Knock-down target sequence #256.  
XX DE

XX ds; RNA production; protein production; drug development;  
XX knock-down target.

XX Unidentified.  
XX OS

XX WO2004094636-A1.  
XX PN

XX 04-NOV-2004.  
XX PD

XX 24-APR-2003; 2003WO-BF004362.  
XX PF

XX 24-APR-2003; 2003WO-BF004362.  
XX PR

PA (GALA-) GALAPAGOS GENOMICS NV.  
 PA (VSCH/) VAN DER SCHUREN J.  
 XX Arts GJF, Lambrecht MJY, Djokic K, Clasen RJ, Mesic E;  
 PI Griffioen S, Bergs CUL;  
 DR WPI; 2004-775940/76.  
 XX  
 XX New knockdown sequences, useful in lowering the amount of RNA and/or  
 PT protein production in cells used in drug development process.  
 PT  
 XX  
 PS Claim 11; SEQ ID NO 259; 402pp; English.  
 XX  
 XX The invention relates to a polynucleotide comprising an RNA sequence. The  
 CC polynucleotides, vector, libraries, and method are useful in lowering the  
 CC amount of RNA and/or protein production in cells used in drug development  
 CC process. The present sequence represents a knock-down target sequence.  
 XX  
 XX Sequence 21 BP; 5 A; 8 C; 1 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 44.8%; Score 13; DB 13; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 GTGATATGCTAGA 17  
 Db 21 GTGATATGCTAGA 9  
 RESULT 14  
 ADQ27975  
 ID ADQ27975 standard; DNA; 24 BP.  
 AC  
 AC ADQ27975;  
 XX  
 XX 09-SEP-2004 (first entry)  
 DT  
 DE Human papillomavirus genotype detection PCR primer #5.  
 XX  
 XX ss: primer; detection; diagnosis; amplification;  
 KW Human Papillomavirus genotype; cervical-neoplasia;  
 KW oncogenic high-risk group.  
 XX  
 XX Human papillomavirus.  
 OS  
 XX WO2004050917-A1.  
 PN  
 XX 17-JUN-2004.  
 PD  
 XX 28-NOV-2003; 2003WO-KR002608.  
 PF  
 XX 29-NOV-2002; 2002KR-00075370.  
 PR  
 XX 31-JUL-2003; 2003KR-00053147.  
 PR  
 XX (ALBI-) ALBIOMED CO.LTD.  
 PA  
 XX Lee S, Kim Y, Yu K, Kim S, Cha K, Ko J;  
 PI  
 XX WPI; 2004-450746/42.  
 DR  
 XX New general primer or primer pair, useful for amplifying and detecting,  
 PT or for use in a nucleic acid amplification process for amplifying Human  
 PT Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV  
 PT genotypes.  
 XX  
 PS Claim 1; SEQ ID NO 5; 71pp; English.  
 XX  
 XX The invention relates to a general primer or primer pair for amplifying  
 CC and detecting or for use in a nucleic acid amplification process for  
 CC amplifying Human Papillomavirus (HPV) genotypes. The general primers are  
 CC useful for amplifying cervical-neoplasia related HPV genotypes including  
 CC oncogenic high-risk groups and low-risk groups. The general primers are  
 CC useful for producing amplifying products to DNA of scores of diverse  
 CC

CC oncogenic HPV types and thus detecting the oncogenic HPV types in a  
 CC sample but also to select cervical carcinoma and its pre-stage lesions at  
 CC early stage by improving sensitivity according to HPV types. This  
 CC sequence corresponds to PCR primer used in the invention.  
 XX  
 SQ Sequence 24 BP; 6 A; 2 C; 7 G; 9 T; 0 U; 0 Other;  
 Query Match 44.8%; Score 13; DB 12; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 17 ATACAGGATTGG 29  
 Db 12 ATACAGGATTGG 24  
 RESULT 15  
 ABN84687  
 ID ABN84687 standard; DNA; 41 BP.  
 XX  
 AC ABN84687;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE HIV-1 amplification primer QAL48.  
 XX  
 XX HIV-1; detection; primer; strand displacement amplification; SDA;  
 KW polymerase; enzyme; pol gene; ss.  
 KW  
 XX Human immunodeficiency virus 1.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_binding 25..41  
 FT /tag= a  
 FT /bound\_moiety= "HIV-1 pol gene"  
 FT /note= "target binding sequence"  
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 PN EP1223227-A2.  
 PD 17-JUL-2002.  
 XX  
 PF 10-DEC-2001; 2001EP-00129200.  
 XX  
 PR 09-JAN-2001; 2001US-00757207.  
 PR  
 PA (BECT ) BECTON DICKINSON & CO.  
 XX  
 XX Hellyer TJ, You Q, Harris JM;  
 PI  
 XX WPI; 2002-620683/67.  
 DR  
 XX Novel oligonucleotide useful for detecting multiple human  
 PT immunodeficiency virus-1 genotypes, has sequence consisting of target  
 PT binding sequence and optionally, a sequence for selected  
 PT amplification/detection reaction.  
 XX  
 PS Claim 1; Page 3; 16pp; English.  
 XX  
 XX The present sequence is that of amplification primer QAL48. This is one  
 CC of a set of claimed amplification and detector primers and probes (see  
 CC ABN84687-723) derived from the HIV-1 polymerase (pol) gene, which  
 CC facilitate the detection and/or quantification of all presently known  
 CC genotypes of HIV-1 (A-1 and O). These primers and probes can be used in a  
 CC variety of amplification and non-amplification formats for the detection  
 CC of HIV nucleic acids. The present primer contains a 3' target binding  
 CC sequence. The remaining 5' portion of the primer comprises a restriction  
 CC endonuclease recognition site that is required for a strand displacement  
 CC amplification (SDA) reaction to proceed, and a generic non-target-  
 CC specific tail sequence. The 'L' in the primer name indicates a 'left'  
 CC primer. The target binding sequence of the primer may alternatively be  
 CC used as a hybridisation probe for direct detection of HIV-1, either  
 CC without prior amplification or as a post-amplification assay. The primers

CC and probes are useful for detecting multiple HIV-1 genotypes, and provide  
 CC real-time detection of HIV-1. (Updated on 29-AUG-2003 to standardise OS  
 CC field)

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 SQ Sequence 41 BP; 10 A; 11 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 44.8%; Score 13; DB 6; Length 41;

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGTAGATACAGGA 24

Db 23 GGTAGATACAGGA 35

Search completed: March 5, 2006, 22:33:21  
 Job time : 275.5 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:12:24 ; Search time 1167.5 Seconds  
(without alignments)  
1411.957 Million cell updates/sec

Title: US-10-720-424B-8

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Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2524774

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Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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14: gb\_htg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 1	14	48.3	69	AY895594	Mus muscu
C 2	13	44.8	31	MMIG23M	X82732 M.musculus
C 3	13	44.8	65	CQ532740	Sequence
C 4	13	44.8	69	AY895739	Mus muscu
C 5	13	44.8	93	CQ144071	Sequence
C 6	13	44.8	93	CQ302512	Sequence
C 7	13	44.8	93	CQ339689	Sequence
C 8	12	41.4	19	AR574640	Sequence
C 9	12	41.4	19	AR574641	Sequence
C 10	12	41.4	19	AR574642	Sequence
C 11	12	41.4	19	AX132750	Sequence
C 12	12	41.4	19	AX132751	Sequence
C 13	12	41.4	19	AX132752	Sequence
C 14	12	41.4	23	CQ855710	Sequence
C 15	12	41.4	23	CQ867591	Sequence
C 16	12	41.4	23	CS000569	Sequence
C 17	12	41.4	50	CS026193	Sequence
C 18	12	41.4	50	CS026202	Sequence

19	12	41.4	51	9	AY895589	AY895589 Mus muscu
C 20	12	41.4	60	6	CQ539360	Sequence
21	12	41.4	65	6	CQ532263	Sequence
22	12	41.4	65	6	CQ555881	Sequence
C 23	12	41.4	65	6	CQ557576	Sequence
C 24	12	41.4	68	6	CQ871437	Sequence
C 25	12	41.4	78	9	AY895820	Mus muscu
C 26	12	41.4	88	2	SV1549277	Septifer
C 27	12	41.4	89	2	LI1549278	AJ549278 Lithophag
28	11	37.9	11	6	CQ837879	Sequence
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C 31	11	37.9	17	6	AX355484	Sequence
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33	11	37.9	17	6	AX672986	Sequence
34	11	37.9	17	6	AX731253	Sequence
35	11	37.9	17	6	AX756776	Sequence
36	11	37.9	17	6	AX758708	Sequence
37	11	37.9	17	6	AX760520	Sequence
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41	11	37.9	18	6	AX838176	Sequence
42	11	37.9	19	6	AR292987	Sequence
C 43	11	37.9	20	6	AR031018	Sequence
C 44	11	37.9	20	6	ARI36805	Sequence
C 45	11	37.9	20	6	ARI39619	Sequence

#### ALIGNMENTS

#### RESULT 1

AY895594/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AY895594  
Mus musculus clone RLS1415D immunoglobulin heavy chain (Igh) mRNA,  
partial cds.  
AY895594  
AY895594.1 GI:62634981

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 69)

Ivanov,I.I., Schelonka,R.L., Zhuang,Y., Gartland,G.L., Zemlin,M.  
and Schroeder,H.W. Jr.

Development of the Expressed Ig CDR-H3 Repertoire Is Marked by  
Focusing of Constraints in Length, Amino Acid Use, and Charge That  
Are First Established in Early B Cell Progenitors

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..69

/organism="Mus musculus"

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/strain="BALB/cJ"

/db\_xref="taxon:10090"

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/gene="Igh"

<1..>69

CDS

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/translation="CARLYGNVAMDYWGQTSVTSS"

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QY 10 GTTACCATGAGCC 23
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Db 21 GTTACCATGAGCC 8

RESULT 2
MMIG23M/c
LOCUS
DEFINITION
M.musculus mRNA for immunoglobulin heavy chain mu VH7183-JH4
(ID:IG23-).
ACCESSION
X82732
VERSION
X82732.1 GI:600654
KEYWORDS
diversity region; immunoglobulin; joining region; N region;
variable region.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 Appasamy,P.M., Weng,Y., Kenniston,T.W., Albert,B.D., DeLeo,B. and
Tang,L.
Expression of diverse and functional TCR V gamma 4 and V gamma 6
transcripts with N region diversity in fetal liver cells cultured
with interleukin 7
Unpublished
JOURNAL
REFERENCE
2 (bases 1 to 31)
AUTHORS
Appasamy,P.M.
TITLE
Direct Submision
JOURNAL
Submitted (10-NOV-1994) P.M. Appasamy, Pittsburgh Cancer Institute,
University of Pittsburgh, Desoto and O'Hara Streets, Pittsburgh,
Pennsylvania PA 15213, USA
FEATURES
Location/Qualifiers
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Db 19 GTTACCATGAGC 7

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LOCUS
DEFINITION
Sequence 2375 from Patent WO0210449.
ACCESSION
CQ532740
VERSION
CQ532740.1 GI:41499004
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
Rattus norvegicus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE
1 Shohan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
Patent: WO 0210449-A 2375 07-FEB-2002;
Compugen Inc. (US)
FEATURES
Location/Qualifiers
source
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QY 13 ACCATAGAGCCAC 25
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Db 34 ACCATAGAGCCAC 22

RESULT 4
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LOCUS
DEFINITION
Mus musculus clone III0428F immunoglobulin heavy chain (Igh) mRNA,
partial cds.
ACCESSION
AY895739
VERSION
AY895739.1 GI:62635271
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 69)
AUTHORS
Ivanov,I.I., Schelonka,R.L., Zhuang,Y., Gartland,G.L., Zemlin,M.
and Schroeder,H.W. Jr.
TITLE
Development of the Expressed Ig CDR-H3 Repertoire Is Marked by
Focusing of Constraints in Length, Amino Acid Use, and Charge That
Are First Established in Early B Cell Progenitors
JOURNAL
J. Immunol. 174 (12), 7773-7780 (2005)
PUBMED
15944280
REFERENCE
2 (bases 1 to 69)
AUTHORS
Ivanov,I.I., Schelonka,R.L., Zhuang,Y., Gartland,L.L., Zemlin,M.
and Schroeder,H.W. Jr.
TITLE
Direct Submision
JOURNAL
Submitted (13-JAN-2005) Departments of Microbiology, Pediatrics and
Medicine, University of Alabama at Birmingham, 1530 3rd Ave S,
Birmingham, AL 35294-3300, USA
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/translation="CARVGYGNLFAYWGQGLTVTWSA"

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 28 AGAGGTTACCATA 16

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LOCUS CQ144071 93 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 14093 from Patent WO0157276.
ACCESSION CQ144071
VERSION CQ144071.1 GI:41101443
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
PENN, S.G., HANZEL, D.K., CHEN, W. and RANK, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 14093 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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/notes="MAP TO AC009225.1
EXPRESSED IN BONE MARROW, SIGNAL = 4.1
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EST_HUMAN HIT: AA091091.1, EVALUE 7.90e-01"

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CQ302512/c
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DEFINITION Sequence 13617 from Patent WO0186003.
ACCESSION CQ302512
VERSION CQ302512.1 GI:41263089
KEYWORDS
SOURCE Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
PENN, S.G., HANZEL, D.K., CHEN, W. and RANK, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 14093 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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Db 58 ATAGAGCCACTAG 46

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DEFINITION Sequence 13783 from Patent WO0157275.
ACCESSION CQ339689
VERSION CQ339689.1 GI:41288760
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
PENN, S.G., HANZEL, D.K., CHEN, W. and RANK, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human brain
Patent: WO 0157275-A 13783 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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QY 16 ATAGAGCCACTAG 28
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Db 58 ATAGAGCCACTAG 46

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DEFINITION Sequence 3968 from patent US 6770633.
ACCESSION AR574640
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VERSION      AR574640.1  GI:56575532
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Robbins,J.M. and Tritz,R.
TITLE        Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL      Patent: US 6770633-A 3968 03-AUG-2004;
             Immusol, Inc.; San Diego, CA
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DEFINITION Sequence 3969 from patent US 6770633.
ACCESSION AR574641
VERSION    AR574641.1  GI:56575533
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS     Robbins,J.M. and Tritz,R.
TITLE       Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL     Patent: US 6770633-A 3969 03-AUG-2004;
             Immusol, Inc.; San Diego, CA
FEATURES    source
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ACCESSION AR574642
VERSION    AR574642.1  GI:56575534
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS     Robbins,J.M. and Tritz,R.
TITLE       Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL     Patent: US 6770633-A 3970 03-AUG-2004;
             Immusol, Inc.; San Diego, CA
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DEFINITION Sequence 3968 from Patent WO0130362.
ACCESSION AR574641
VERSION    AR574641.1  GI:14139055
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE  1
AUTHORS     Robbins,J.M. and Tritz,R.
TITLE       Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL     Patent: WO 0130362-A 3968 03-MAY-2001;
             IMMUSOL, INC. (US)
FEATURES    source
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Db
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DEFINITION Sequence 3969 from Patent WO0130362.
ACCESSION AR574641
VERSION    AR574641.1  GI:14139056
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE  1
AUTHORS     Robbins,J.M. and Tritz,R.
TITLE       Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL     Patent: WO 0130362-A 3969 03-MAY-2001;
             IMMUSOL, INC. (US)
FEATURES    source
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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666.144 Million cell updates/sec

Title: US-10-720-424B-1

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Sequence: 1 gatggtgatgtgtagatcacaggatttgg 29

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Gapop 60.0 , Gapext 60.0

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9: /cgn2\_6/prodata/1/pubpna/US10E\_PUBCOMB.seq:  
10: /cgn2\_6/prodata/1/pubpna/US11\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	29	8 US-10-720-424B-1	Sequence 1, Appli
2	15	51.7	25	8 US-10-719-900-207943	Sequence 207943,
3	15	51.7	25	8 US-10-719-900-473578	Sequence 473578,
4	15	51.7	25	8 US-10-719-900-493325	Sequence 493325,
5	15	51.7	25	10 US-11-036-317-670021	Sequence 670021,
6	14	48.3	25	5 US-10-098-263B-16386	Sequence 16386, A
7	14	48.3	25	7 US-10-719-956-350520	Sequence 350520,
8	13	44.8	25	8 US-10-257-017B-176713	Sequence 176713,
9	13	44.8	13	8 US-10-257-017B-176714	Sequence 176714,
10	13	44.8	17	3 US-09-927-046-382	Sequence 382, App
11	13	44.8	17	3 US-09-927-046-1794	Sequence 1794, Ap
12	13	44.8	17	3 US-09-927-046-2111	Sequence 2111, Ap
13	13	44.8	24	8 US-10-720-424B-5	Sequence 5, Appli
14	13	44.8	25	7 US-10-681-773-3553	Sequence 3553, Ap
15	13	44.8	25	7 US-10-681-773-60170	Sequence 60170, A
16	13	44.8	25	7 US-10-681-773-87785	Sequence 87785, A
17	13	44.8	25	7 US-10-681-773-98759	Sequence 98759, A
18	13	44.8	25	7 US-10-681-773-99269	Sequence 99269, A
19	13	44.8	25	7 US-10-719-956-16054	Sequence 16054, A
20	13	44.8	25	7 US-10-719-956-290994	Sequence 290994,
21	13	44.8	25	7 US-10-719-956-533125	Sequence 533125,
22	13	44.8	25	8 US-10-719-900-350776	Sequence 350776,
23	13	44.8	25	8 US-10-719-900-375428	Sequence 375428,

c	24	13	44.8	25	8 US-10-719-900-453770	Sequence 453770,
c	25	13	44.8	25	8 US-10-719-900-919771	Sequence 919771,
c	26	13	44.8	25	9 US-10-956-157-117633	Sequence 117633,
c	27	13	44.8	25	9 US-10-956-157-117638	Sequence 117638,
c	28	13	44.8	25	9 US-10-956-157-117639	Sequence 117639,
c	29	13	44.8	25	9 US-10-956-157-223019	Sequence 223019,
c	30	13	44.8	25	9 US-10-956-157-224989	Sequence 224989,
c	31	13	44.8	25	9 US-10-843-527-79313	Sequence 79313, A
c	32	13	44.8	25	9 US-10-843-527-158864	Sequence 158864,
c	33	13	44.8	25	10 US-11-036-317-759047	Sequence 759047,
c	34	13	44.8	25	10 US-11-060-756-35453	Sequence 35453, A
c	35	13	44.8	25	10 US-11-060-756-35457	Sequence 35457, A
c	36	13	44.8	25	10 US-11-060-756-35481	Sequence 35481, A
c	37	13	44.8	25	10 US-11-060-756-57112	Sequence 57112, A
c	38	13	44.8	25	10 US-11-060-756-57116	Sequence 57116, A
c	39	13	44.8	25	10 US-11-060-756-57117	Sequence 57117, A
c	40	13	44.8	25	10 US-11-060-756-57119	Sequence 57119, A
c	41	13	44.8	25	10 US-11-060-756-294352	Sequence 294352,
c	42	13	44.8	41	3 US-09-757-207-1	Sequence 1, Appli
c	43	13	44.8	46	6 US-10-294-957-21	Sequence 21, Appl
c	44	12	41.4	17	3 US-09-927-046-383	Sequence 383, App
c	45	12	41.4	17	3 US-09-927-046-1572	Sequence 1572, Ap

ALIGNMENTS

RESULT 1  
US-10-720-424B-1  
; Sequence 1, Application US/10720424B  
; Publication No. US20040248085A1  
; GENERAL INFORMATION:  
; APPLICANT: ALBIONED CO., LTD  
; APPLICANT: Lee, Sang-Wha  
; APPLICANT: Kim, Yeon-Soo  
; APPLICANT: Yu, Kang-Yeol  
; APPLICANT: Kim, Seung-Jo  
; APPLICANT: Cha, Kwang-Yul  
; APPLICANT: Ko, Jung-Jae  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR  
; FILE REFERENCE: NEI0018  
; CURRENT APPLICATION NUMBER: US/10/720,424B  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: KR10-2002-0075370  
; PRIOR FILING DATE: 2002-11-29  
; PRIOR APPLICATION NUMBER: KR10-2003-0053147  
; PRIOR FILING DATE: 2003-07-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Human Papillomavirus  
US-10-720-424B-1  
Query Match 100.0%; Score 29; DB 8; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06; Indels 0; Gaps 0;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GATGCTGATGCTGATGATACAGGATTTCG 29  
Db 1 GATGCTGATGCTGATGATACAGGATTTCG 29  
RESULT 2  
US-10-719-900-207943  
; Sequence 207943, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1



; CURRENT APPLICATION NUMBER: US/10/719,956  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 350520  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-719-956-350520

Query Match 48.3%; Score 14; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGTGATATGGTAG 17  
|||||  
DB 18 GGTGATATGGTAG 5

## RESULT 8

US-10-257-017B-176713  
; Sequence 176713, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 176713  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043853  
US-10-257-017B-176713

Query Match 44.8%; Score 13; DB 8; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGTGATATGGTAG 16  
|||||  
DB 1 GGTGATATGGTAG 13

## RESULT 9

US-10-257-017B-176714/c  
; Sequence 176714, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 176714  
; LENGTH: 13  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043853  
US-10-257-017B-176714

Query Match 44.8%; Score 13; DB 8; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGTGATATGGTAG 16  
|||||  
DB 13 GGTGATATGGTAG 1

## RESULT 10

US-09-927-046-382  
; Sequence 382, Application US/09927046  
; Publication No. US20030064946A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Thompson, Jim  
; APPLICANT: McKenzie, Tim  
; APPLICANT: Avers, Dave  
; APPLICANT: Grupe, Andrew  
; APPLICANT: Szymkowski, Edmund  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlor  
; FILE REFERENCE: 249/021  
; CURRENT APPLICATION NUMBER: US/09/927,046  
; CURRENT FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 5450  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 382  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-927-046-382

Query Match 44.8%; Score 13; DB 3; Length 17;  
Best Local Similarity 76.9%; Pred. No. 1.8e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGTGATAGTACAG 22  
|:|:|:|:|:|:|  
DB 4 AUGGUAGUACAG 16

## RESULT 11

US-09-927-046-1794  
; Sequence 1794, Application US/09927046  
; Publication No. US20030064946A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Thompson, Jim  
; APPLICANT: McKenzie, Tim  
; APPLICANT: Avers, Dave  
; APPLICANT: Grupe, Andrew  
; APPLICANT: Szymkowski, Edmund  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlor  
; FILE REFERENCE: 249/021  
; CURRENT APPLICATION NUMBER: US/09/927,046  
; CURRENT FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 5450  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1794  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-927-046-1794

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Query Match          44.8%; Score 13; DB 3; Length 17;
Best Local Similarity 76.9%; Pred. No. 1.8e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGGTAGATACAG 22
   |||:|||||
Db 2 AUGGUAGAUACAG 14

RESULT 12
US-09-927-046-2111
; Sequence 2111, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2111
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-2111

Query Match          44.8%; Score 13; DB 3; Length 17;
Best Local Similarity 76.9%; Pred. No. 1.8e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGGTAGATACAG 22
   |||:|||||
Db 3 AUGGUAGAUACAG 15

RESULT 13
US-10-720-424B-5
; Sequence 5, Application US/10720424B
; Publication No. US20040248085A1
; GENERAL INFORMATION:
; APPLICANT: ALBIONED CO., LTD
; APPLICANT: Lee, Sang-wha
; APPLICANT: Kim, Yeon-soo
; APPLICANT: Yu, Kang-yeol
; APPLICANT: Kim, Seung-jo
; APPLICANT: Cha, Kwang-yul
; APPLICANT: Ko, Jung-jae
; TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
; FILE REFERENCE: NEIT0018
; CURRENT APPLICATION NUMBER: US/10/720,424B
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: KR10-2002-0075370
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: KR10-2003-0053147
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Human Papillomavirus
US-10-720-424B-5

Query Match          44.8%; Score 13; DB 8; Length 24;
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ATACAGGATTTGG 29
   |||:|||||
Db 12 ATACAGGATTTGG 24

RESULT 14
US-10-681-773-3553/c
; Sequence 3553, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 3553
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-3553

Query Match          44.8%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AGATACAGGATTT 27
   |||:|||||
Db 13 AGATACAGGATTT 1

RESULT 15
US-10-681-773-60170/c
; Sequence 60170, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 60170
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-60170

Query Match          44.8%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AGATACAGGATTT 27
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Db 19 AGATACAGGATT 7

Search completed: March 5, 2006, 23:01:34  
Job time : 361 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
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C 2	13	44.8	55	11	CR260472	CR260472 Forward S
C 3	13	44.8	66	9	BZ291460	BZ291460 SALK_1207
C 4	13	44.8	62	14	BG932614	BG932614 h81-64 h8
C 5	13	44.8	85	9	AZ919663	AZ919663 1006016B0
C 6	13	44.8	85	9	CR274455	CR274455 mai69c08.
C 7	13	44.8	100	7	CN563098	CN563098 taf83b02.
C 8	12	41.4	41	7	CO740007	CO740007 SILB06a25
C 9	12	41.4	43	10	CZ911033	CZ911033 4012004G0
C 10	12	41.4	46	7	CO735002	CO735002 SLLE04c10
C 11	12	41.4	46	9	BH864657	BH864657 SALK_0965
C 12	12	41.4	52	11	CR357756	CR357756 AraEidops
C 13	12	41.4	53	9	B02637	B02637 CSRL-157G5-
C 14	12	41.4	54	9	AZ435736	AZ435736 IM0080M03
C 15	12	41.4	61	1	AA585225	AA585225 KTH167 HT
C 16	12	41.4	61	9	AZ829961	AZ829961 2M0107122
C 17	12	41.4	64	1	A1289007	A1289007 q186h06.x
C 18	12	41.4	64	3	EM285347	EM285347 pb12S06.y
C 19	12	41.4	66	1	AV770608	AV770608 AV770608
C 20	12	41.4	69	9	AZ276708	AZ276708 IM00566B01
C 21	12	41.4	73	3	BP916081	BP916081 BP916081
C 22	12	41.4	71	10	CG522729	CG522729 OST92779

10

/note="Organ: Breast; Vector: pAmp-1; 3' RACE of total RNA from genetrapp pools; shotgun clone in pAmp-1 and used to transform DH5-alpha competent bacteria."

ORIGIN

Query Match 48.3%; Score 14; DB 9; Length 74;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GATATGGTAGATAC 20  
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Db 63 GATATGGTAGATAC 50

RESULT 2  
CR260472/c  
LOCUS  
DEFINITION  
Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN342d22, genomic survey sequence.  
CR260472  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CR260472.1 GI:50039325  
GSS; genome survey sequence; MICER.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.  
TITLE  
Direct Submision  
JOURNAL  
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER

FEATURES  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPN342d22"  
/clone\_lib="MHPN"

ORIGIN

Query Match 44.8%; Score 13; DB 11; Length 55;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGGTAGATACAG 22  
|||||  
Db 15 ATGGTAGATACAG 3

RESULT 3  
BZ291460  
LOCUS  
DEFINITION  
SALK\_120782.34.65.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_120782.34.65.x, genomic survey sequence.  
BZ291460  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
AUTHORS  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.  
TITLE  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
JOURNAL  
Unpublished (2001)

## COMMENT

Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckergsaalk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At3g4720.  
Class: TDNA tagged.

FEATURES  
source

Location/Qualifiers  
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/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna\_protocols.html"

## ORIGIN

Query Match 44.8%; Score 13; DB 9; Length 66;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGGTCATATGGTA 15  
|||||  
Db 29 TGGTCATATGGTA 41

## RESULT 4

BG932614/c  
LOCUS  
DEFINITION  
h81-64 h81 S. mansoni adult mini-library, Fietto/DeMarco/Verjovski-Almeida Schistosoma mansoni cDNA, mRNA sequence.  
BG932614  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Schistosoma mansoni  
Schistosoma mansoni  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.  
REFERENCE  
AUTHORS  
Fietto,J.L.R., DeMarco,R. and Verjovski-Almeida,S.  
TITLE  
Use of degenerate primers and touchdown PCR for construction of cDNA libraries  
JOURNAL  
Biotechniques 32 (6), 1404-1408 (2002)

COMMENT  
Contact: Verjovski-Almeida S  
Departamento de Bioquímica, Instituto de Química  
Universidade de Sao Paulo  
Av. Lineu Prestes, 748, Sao Paulo, SP 05508-900, Brasil  
Tel: 55-11-3091-2173  
Fax: 55-11-3091-2186  
Email: verjo@iq.usp.br.

FEATURES  
source

Location/Qualifiers  
1..83  
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/mol\_type="mRNA"  
/strain="BH"  
/db\_xref="taxon:6183"  
/dev\_stage="Adult"  
/clone\_lib="h81 S. mansoni adult mini-library, Fietto/DeMarco/Verjovski-Almeida"  
/note="Vector: Bluescript SK; minilibrary constructed using low-stringency RT-PCR and consensus-degenerate primer"

## ORIGIN

Query Match 44.8%; Score 13; DB 2; Length 83;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ATACAGGATTGGS 29  
 |||||  
 Db 13 ATACAGGATTGGS 1

## RESULT 5

AZ919663

LOCUS

DEFINITION 85 bp DNA linear GSS 17-DEC-2001  
 1006016804.x1 1006 - RescueMu Grid G Zea mays genomic, genomic  
 survey sequence.

ACCESSION AZ919663

VERSION AZ919663.1

KEYWORDS GSS

SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 85)

AUTHORS Walbot,V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished (2001)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1006016 row: 41

Class: transposon-tagged.

## FEATURES

source

1..85

/organism="Zea mays"

/mol\_type="genomic DNA"

/culivar="mixed background W23/A198/B73"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="1006 - RescueMu Grid G"

/note="Organ: leaf; Vector: RescueMu (engineered from  
 pBluescript backbone); Site\_1: BamHI; Site\_2: BglII;  
 RescueMu is a 4.9 kb, modified maize Mu transposon.  
 Designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription  
 units. For more information on RescueMu, go to the web  
 site 'www.znldb.iastate.edu' and follow the links for  
 'RescueMu'. Grid G was grown at Stanford in 2000. DNA was  
 extracted from leaf punches, double digested using BamHI  
 and BglII, and ligated to form circular plasmids. DH10B  
 cells were transformed and then screened on LB plates with  
 ampicillin."

## ORIGIN

Query Match 44.8%; Score 13; DB 9; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGGTAGATACAG 22  
 |||||  
 Db 6 ATGGTAGATACAG 18

## RESULT 6

CB274455/c

LOCUS

99 bp mRNA linear EST 24-FEB-2003

## DEFINITION

ma169c08.y1 McCarrey Eddy spermatocytes Mus musculus cDNA clone  
 IMAGE:6446702 5', mRNA sequence.

## ACCESSION

CB274455

## VERSION

CB274455.1

## KEYWORDS

EST.

## SOURCE

Mus musculus

## ORGANISM

Mus musculus (house mouse)

## REFERENCE

1 (bases 1 to 99)

AUTHORS

McCarrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Pape,D.,  
 Martin,J., Wylie,T., Dente,M., Bowers,Y., Theising,B., Gibbons,M.,  
 Ritter,E., Tagareishvili,R., Ronkoi,L., Maguire,L., Kennedy,S.,  
 Bennett,J., Waterston,R. and Wilson,R.

NIEHS Mouse

Unpublished (2002)

COMMENT

Contact: McCarrey/Eddy NIEHS Mouse

NIEHS Mouse

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Library constructed and donated by J. McCarrey, Ph.D. (Southwest

Foundation for Biomedical Research, Dept. of Genetics) - excision

done by E.M. Eddy, Ph.D. (National Institutes of Health, National

Institute of Environmental Health Sciences).

MGI:2070662

Seq primer: Primer name ambiguous.

Location/Qualifiers

1..99

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="CD-1"

/db\_xref="taxon:10090"

/clone="IMAGE:6446702"

/sex="male"

/tissue\_type="spermatocytes, pooled from multiple mice"

/dev\_stage="60 day"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="McCarrey Eddy spermatocytes"

/note="Organ: testis; Vector: pBluescript SK+

(Stratagene); Site\_1: XhoI; Site\_2: EcoRI; cDNA oligo

dt-primed [5'-(GA)10-ACGAGTCGAGTGTGTTT-3'] and

directionally cloned using 5' linkers 5'-AATCGGCACGAG-3'

and 5'-CTCGTGGCG-3'. Size selection of >400bp material

gives average insert size ranging from 1-2 kb. Library was

single-stranded phagmids were prepped and transformed

into DH10B. Library contains 98% recombinants.

References: J. Androl. 20:635-639 and Gene 25:263-269.

Library constructed and donated by J. McCarrey, Ph.D.

(Southwest Foundation for Biomedical Research, Dept. of

Genetics); excision done by E.M. Eddy, Ph.D. (National

Institutes of Health, National Institute of Environmental

Health Sciences). Original lambda-based library is

available through ATCC, catalog #63422."

## ORIGIN

Query Match 44.8%; Score 13; DB 6; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGGTGATATGCTA 15  
 |||||  
 Db 62 TGGTGATATGCTA 50

## RESULT 7

CNS563098/c

LOCUS

DEFINITION

tat83b02.x2 Hydra EST -Kiel 1 Hydra magnipapillata cDNA 3' similar

100 bp mRNA linear EST 03-MAY-2004

to SW:RLA2\_BRAF1 001725 60S ACIDIC RIBOSOMAL PROTEIN P2. ;, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CN563098 GI:46972402

Hydra magnipapillata

Hydra magnipapillata

Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydroids; Anthomedusae; Hydridae; Hydra.

1 (bases 1 to 100)

REFERENCE

AUTHORS

Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q., Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagarishvili,R., Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.

WashU Hydra EST Project

Unpublished (2002)

TITLE

JOURNAL

COMMENT

Other ESTs: taf83b02.y2

Contact: Hans Bode

WashU Hydra EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

Library was constructed by Konstantin Khalturin, Zoologisches Institut, Univ. Kiel, Germany Library materials provided by Thomas Bosch, Zoologisches Institut, CAU Kiel, Germany DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Hans Bode (hrobode@uci.edu)

Putative full length read

vector to vector length is

Seq primer: degenerate primer.

Location/Qualifiers

FEATURES

source

1..100

/organism="Hydra magnipapillata"

/mol\_type="mRNA"

/strain="105"

/db\_xref="taxon:6085"

/lab\_host="DH5a"

/clone\_lib="Hydra EST -Kiel 1"

/notes="Vector: pSPORT1; Site 1: Not I; Site 2: Sal I;

pSPORT 1 Vector is ampicillin resistant, M13 reverse

primer was used by us for sequencing of 5' parts of

inserts; 3' parts of cDNAs contain long polyA tracks which

makes sequencing from 3' direction complicated"

ORIGIN

Query Match 44.8%; Score 13; DB 7; Length 100;

Best Local Similarity 100.0%; Pred. No. 6.9e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGGTGATATGG 13

|||||

27 GATGGTGATATGG 15

RESULT 8

LOCUS

DEFINITION

clone 25103 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Spermophilus lateralis (golden-mantled ground squirrel)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Scuriidae; Xerinae; Marmotini; Spermophilus.

1 (bases 1 to 41)

REFERENCE

AUTHORS

Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W.,

Rogers,J. and Cossins,A.R.

TITLE

JOURNAL

COMMENT

Unpublished (2004)

Contact: Andrew R. Cossins

Laboratory for Environmental Gene Regulation

University of Liverpool

School of Biological Sciences, The Biosciences Building, Crown

Street, Liverpool, United Kingdom, L69 7ZB

Tel: +44(0)151-795-4510

Fax: +44(0)151-795-4431

Email: cossins@liv.ac.uk

Vector has been trimmed from this EST.

Plate: 25 row: 1 column: 03

Seq primer: triplex 5'LD (5'-CTCGGAAGCGGCCCATGTGTGTGT-3')

High quality sequence stop: 41.

FEATURES

source

1..41

/organism="Spermophilus lateralis"

/mol\_type="mRNA"

/db\_xref="taxon:76772"

/clone="25103"

/sex="Male & female"

/tissue type="brain"

/dev stage="Adult"

/lab\_host="E.coli Electromax DH10B"

/clone\_lib="squirrel brain library 1"

/note="Vector: pTriplex2; Site 1: SfiI GGCCATTACGGCC;

Site 2: SfiI GGCCGCTCGGCC; Normalized cDNA library

prepared from brain of hibernating and summer animals"

ORIGIN

Query Match 41.4%; Score 12; DB 7; Length 41;

Best Local Similarity 100.0%; Pred. No. 2.6e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGTGATATGGTA 15

|||||

14 GGTGATATGGTA 3

RESULT 9

LOCUS

DEFINITION

survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 43)

Walbot,V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4012004 column: 2

Class: transposon-tagged

Location/Qualifiers

1..43

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="4012 - RescueMu Grid BB"  
 /note="Organ: leaf; Vector: RescueMu (engineered from plusScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid BB was grown at UC Berkeley in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 41.4%; Score 12; DB 10; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGTAGATACAG 22  
 |||||  
 Db 32 TGTAGATACAG 43

RESULT 10  
 C0735002/c

LOCUS  
 DEFINITION  
 SLL504c10g02f1 squirrel embryo library 1 Sperophilus lateralis  
 cDNA clone 10g02 5', mRNA sequence.

ACCESSION  
 VERSION  
 C0735002  
 C0735002.1 GI:50822272

KEYWORDS  
 SOURCE  
 ORGANISM

Sperophilus lateralis (golden-mantled ground squirrel)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Scuridae; Xerinae; Marmotini; Sperophilus.

REFERENCE  
 1 (bases 1 to 46)

AUTHORS  
 Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,

Rogers, J., and Cossins, A.R.  
 Microarray analysis of transcriptional changes during hibernation  
 in the golden mantled ground squirrel, *Sperophilus lateralis*

UNPUBLISHED (2004)

Contact: Andrew R. Cossins

Laboratory for Environmental Gene Regulation  
 University of Liverpool  
 School of Biological Sciences, The Biosciences Building, Crown  
 Street, Liverpool, United Kingdom, L69 7ZB

Tel: +44(0)151-795-4510

Fax: +44(0)151-795-4431

Email: cossins@liverpool.ac.uk

Vector has been trimmed from this EST.

Plate: 10 row: 9 column: 02

Seq primer: pf1c T7 (5'-AATACGACTCACTATAGG-3')

High quality sequence stop: 46.

## FEATURES

source

1..46

/organism="Sperophilus lateralis"

/mol\_type="mRNA"

/db\_xref="taxon:76772"

/clone="10g02"

/sex="male and female"

/tissue\_type="embryo"

/dev\_stage="embryonic"

/lab\_host="E.coli Electromax DH10B"

/clone\_lib="squirrel embryo library 1"

/note="Vector: pf1c; Site 1: SalI GTCGAG; Site 2: BamHI

GATCC; Normalized and subtracted cDNA library prepared

from embryos"

## ORIGIN

Query Match 41.4%; Score 12; DB 7; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GTAGATACAGGA 24  
 |||||  
 Db 17 GTAGATACAGGA 6

RESULT 11

BH864657

LOCUS

DEFINITION

Arabidopsis thaliana

genomic clone SALK\_096549, genomic survey sequence.

ACCESSION

VERSION

BH864657.1 GI:22100555

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 46)

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmermann, J., and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

UNPUBLISHED (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salilab.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At1g79990.

Class: TDNA tagged.

Location/Qualifiers

1..46

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/ecotype="Col-0"

/db\_xref="taxon:3702"

/clone="SALK\_096549"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 41.4%; Score 12; DB 9; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GTAGATACAGGA 24  
 |||||  
 Db 19 GTAGATACAGGA 30

RESULT 12

CR357756/c

LOCUS

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence GK-722B11-025199,

genomic survey sequence.

ACCESSION

VERSION

CR357756.1 GI:45540678

Query Match 41.4%; Score 12; DB 9; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GTAGATACAGGA 24

Db 19 GTAGATACAGGA 30

RESULT 12

CR357756

LOCUS

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence GK-722B11-025199,

genomic survey sequence.

ACCESSION

VERSION

CR357756.1 GI:45540678

KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE  
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehovever, P. and Weisshaar, B.  
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)  
PUBMED 12874060

REFERENCE  
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-kat) for flanking sequence tag-based reverse genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
PUBMED 14756321

REFERENCE  
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehovever, P., Dekker, K.A. and Weisshaar, B.  
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL Biotechniques 35 (6), 1164-1168 (2003)  
PUBMED 14682050

REFERENCE  
AUTHORS Strizhov, N., Li, Y., Rosso, M.G. and Weisshaar, B.  
TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT It indicates an insertion within the locus defined by BAC clone F9D24. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-kat project. GABI-kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES  
source Location/Qualifiers  
1..52  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-722B11-025198"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/scotyle="Col-0"  
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pGAB1 (GenBank accession number: AY529716). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN  
Query Match 41.4%; Score 12; DB 11; Length 52;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGGTAGATACA 21  
|||||  
Db 34 ATGGTAGATACA 23

RESULT 13  
B02637/c 53 bp DNA linear GSS 13-JUL-1996  
LOCUS CSRL-157G6-u CSRL flow sorted Chromosome 11 specific cosmid Homo  
DEFINITION sapiens genomic clone CSRL-157G6, genomic survey sequence.

ACCESSION B02637  
VERSION B02637.1 GI:1411915

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Evans, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M., Jones, D., Ward, T., Gillilan, E., Schagemann, J., Probst, S., Harris, J., DeFord, J., McFarland, J., Burzinski, K., Khan, M., Kupfer, K. and Garner, H.R.  
TITLE Genomic Sequence Sampled Map of Chromosome 11

JOURNAL Unpublished (1996)  
COMMENT Contact: Evans GA, Shane Probst  
McDermott Center for Human Growth and Development  
University of Texas Southwestern Medical Center At Dallas  
5323 Harry Hines Blvd, Dallas TX 75235-8591  
Tel: 214-648-1600  
Fax: 214-648-1666  
Email: [gevans@utsw.swmed.edu](mailto:gevans@utsw.swmed.edu), [shane@mcdermott.swmed.edu](mailto:shane@mcdermott.swmed.edu)  
Seq primer: T7  
Class: cosmid ends  
High quality sequence stop: 53.  
Location/Qualifiers  
1..53  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="CSRL-157G6"  
/sex="female"  
/cell\_type="chimeric hamster somatic cell hybrid"  
/clone\_lib="CSRL flow sorted Chromosome 11 specific cosmid"  
/note="Vector: sCos-1; Human Chromosome 11 specific cosmid library prepared from flow sorted human Chromosome 11 derived from Chinese Hamster Ovary (CHO) monochromosomal somatic cell hybrid, J1"

ORIGIN  
Query Match 41.4%; Score 12; DB 9; Length 53;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TAGATACAGGAT 25  
|||||  
Db 17 TAGATACAGGAT 6

RESULT 14  
AZ345736/c 54 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0080M03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0080M03 R, genomic survey sequence.

ACCESSION AZ345736  
VERSION AZ345736.1 GI:10424973

KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.  
TITLE 1 (bases 1 to 54)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT



84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: M column: 03  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 54.

## FEATURES

source

1. .54  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080M03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb Plasmid UUGC1M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 41.4%; Score 12; DB 9; Length 54;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGATATGGTAGA 17

Db 23 TGATATGGTAGA 12

## RESULT 15

AA585225

LOCUS

KTH167 HTCDL1 Homo sapiens cDNA 5'3', mRNA sequence. EST 09-SEP-1997

AA585225

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 61)

Sohn, U., Park, D.S., Lee, C.M., Cho, W.K., Ahn, H.J., Lee, M.Y.,

Hwang, M.Y. and Jin, S.W.

Human HTCDL1 library cDNAs

Unpublished (1994)

Contact: Uik

Sohn, D.S. Park, C.M. Lee, W.K. Cho, H.J. Ahn, M.Y. Lee, M.Y. Hwang, S.W. Jin

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Kyungpook National University

Dept. of Genetic Eng., Kyungpook National Univ., Taegu 702-701,

Korea

Tel: 82-053-950-5382

Fax: 82-053-955-5327  
Email: usohn@bh.kyungpook.ac.kr  
Seq primer: M13 Reverse/SK primer.

## FEATURES

source

1. .61  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/lab\_host="XL1-Blue"  
/clone\_lib="HTCDL1"  
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: EcoRI; Poly(A)-mRNA from the 2-year-old male fetal thymus, oligo(dT) priming, EcoRI cloning in the vector pBluescript (Stratagene)."

## ORIGIN

Query Match 41.4%; Score 12; DB 1; Length 61;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGATATGGTAG 16

Db 21 GTGATATGGTAG 32

Search completed: March 6, 2006, 00:16:49  
Job time : 2991.5 secs

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3	14	48.3	19	11	US-11-101-244-1492736	Sequence 1492736,
C	14	48.3	25	12	US-11-083-784-1492736	Sequence 276816,
	14	48.3	25	12	US-11-121-849-276816	Sequence 93016, A
5	14	48.3	30	12	US-11-175-859-93016	Sequence 662756,
6	13	44.8	19	10	US-11-101-244-662756	Sequence 662756,
7	13	44.8	19	10	US-11-101-244-662769	Sequence 662769,
C	13	44.8	19	10	US-11-101-244-662769	Sequence 1366068,
	13	44.8	19	10	US-11-101-244-1379350	Sequence 1379350,
9	10	44.8	19	10	US-11-101-244-1492657	Sequence 1492657,
10	13	44.8	19	10	US-11-101-244-1492657	Sequence 1492657,
11	13	44.8	19	11	US-11-083-784-662756	Sequence 662756,
12	13	44.8	19	11	US-11-083-784-662769	Sequence 662769,
C	13	44.8	19	11	US-11-083-784-1366068	Sequence 1366068,
	13	44.8	19	11	US-11-083-784-1379350	Sequence 1379350,
14	13	44.8	19	11	US-11-083-784-1492657	Sequence 1492657,
15	13	44.8	21	7	US-10-537-002-67	Sequence 67, Appl
16	13	44.8	25	12	US-11-121-849-38480	Sequence 38480,
C	17	44.8	25	12	US-11-121-849-385027	Sequence 385027,
	13	44.8	25	12	US-11-121-849-480659	Sequence 480659,
C	19	44.8	25	12	US-11-121-849-512932	Sequence 512932,
C	20	44.8	25	12	US-11-121-849-512932	Sequence 512932,

US-11-101-244-1492736  
 ; Sequence 1492736, Application US/11/101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyper  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/101-244

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; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1492736
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1492736

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Best Local Similarity 78.6%; Pred. No. 85;
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Db      4 GGUAUAUACAGGAU 17
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; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1492736
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1492736

Query Match      48.3%; Score 14; DB 11; Length 19;
Best Local Similarity 78.6%; Pred. No. 85;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      12 GGTAGATACAGGAT 25
Db      4 GGUAUAUACAGGAU 17
      ||:||||:||||:

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; Sequence 276816, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
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; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 276816
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-276816

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Best Local Similarity 100.0%; Pred. No. 86;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GGTGATATGGTAGA 17
Db      15 GGTGATATGGTAGA 2
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RESULT 5
US-11-175-859-93016
; Sequence 93016, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 93016
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-93016

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Best Local Similarity 100.0%; Pred. No. 88;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GATGGTATATGGT 14
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RESULT 6
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; Sequence 662756, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 662756
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-662756
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Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GUAGAUACAGGAU 13

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US-11-083-784-662756  
; Sequence 662756, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 662756  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-662756

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Best Local Similarity 76.9%; Pred. No. 3.3e+02;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGGTAGATACAG 22  
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Db 4 AUGGAGAUACAG 16

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US-11-083-784-662769  
; Sequence 662769, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
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; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
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; TYPE: RNA  
; ORGANISM: Homo sapiens

## US-11-083-784-662769

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Db 5 AUGGAGAUACAG 17

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; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
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US-11-083-784-1366068

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US-11-083-784-1379350  
; Sequence 1379350, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
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; SOFTWARE: Proprietary  
; SEQ ID NO 1379350

; LENGTH: 19  
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; ORGANISM: Homo sapiens  
US-11-083-784-1379350

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Best Local Similarity 69.2%; Pred. No. 3.3e+02;  
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QY 14 TAGATACAGGATT 26  
Db 6 UAGAUACAGGAU 18

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; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1492657  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1492657

Query Match 44.8%; Score 13; DB 11; Length 19;  
Best Local Similarity 76.9%; Pred. No. 3.3e+02;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 GTAGATACAGGAT 25  
Db 1 GUAGAUACAGGAU 13

Search completed: March 5, 2006, 22:48:29  
Job time : 450.5 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 19:08:04 ; Search time 78 Seconds  
(without alignments)  
660.888 Million cell updates/sec

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Searched: 1303057 seqs, 888780828 residues

Word-size: 10

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Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/PCUTS COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 5	12	41.4	21	US-09-090-947-13	Sequence 13, Appl
6	12	41.4	25	US-09-396-196G-36348	Sequence 36348, A
C 7	12	41.4	25	US-09-396-196G-73518	Sequence 73518, A
C 8	12	41.4	25	US-09-396-196G-73519	Sequence 73519, A
C 9	12	41.4	25	US-09-396-196G-81905	Sequence 81905, A
C 10	12	41.4	25	US-09-396-196G-94653	Sequence 94653, A
C 11	12	41.4	25	US-09-396-196G-94664	Sequence 94664, A
C 12	12	41.4	25	US-09-396-196G-94665	Sequence 94665, A
C 13	12	41.4	98	US-09-513-999C-22225	Sequence 22225, A
C 14	11	37.9	20	US-09-021-701-1077	Sequence 1077, Ap
C 15	11	37.9	20	US-09-021-701-1078	Sequence 1078, Ap
C 16	11	37.9	20	US-09-021-701-1079	Sequence 1079, Ap
C 17	11	37.9	20	US-09-021-701-1080	Sequence 1080, Ap
C 18	11	37.9	20	US-09-021-701-1081	Sequence 1081, Ap
C 19	11	37.9	20	US-09-021-701-1082	Sequence 1082, Ap
C 20	11	37.9	20	US-09-021-701-1083	Sequence 1083, Ap
C 21	11	37.9	20	US-09-021-701-1084	Sequence 1084, Ap
C 22	11	37.9	20	US-09-021-701-1085	Sequence 1085, Ap
C 23	11	37.9	20	US-09-021-701-1086	Sequence 1086, Ap
C 24	11	37.9	20	US-09-363-970-11	Sequence 11, Appl

C 25	11	37.9	20	US-09-198-452A-2044	Sequence 2044, Ap
26	11	37.9	22	US-09-612-204B-30	Sequence 30, Appl
27	11	37.9	22	US-10-055-364-30	Sequence 30, Appl
28	11	37.9	24	US-08-828-952-2	Sequence 2, Appl
C 29	11	37.9	25	US-09-396-196G-32627	Sequence 32627, A
C 30	11	37.9	25	US-09-396-196G-32638	Sequence 32638, A
C 31	11	37.9	25	US-09-396-196G-32639	Sequence 32639, A
C 32	11	37.9	25	US-09-396-196G-32640	Sequence 32640, A
C 33	11	37.9	25	US-09-396-196G-32641	Sequence 32641, A
C 34	11	37.9	25	US-09-396-196G-43128	Sequence 43128, A
C 35	11	37.9	25	US-09-396-196G-43129	Sequence 43129, A
C 36	11	37.9	25	US-09-396-196G-73517	Sequence 73517, A
C 37	11	37.9	25	US-09-396-196G-120975	Sequence 120975, A
C 38	11	37.9	25	US-09-396-196G-120976	Sequence 120976, A
C 39	11	37.9	25	US-09-396-196G-120977	Sequence 120977, A
C 40	11	37.9	25	US-09-396-196G-120978	Sequence 120978, A
C 41	11	37.9	25	US-10-002-623-348	Sequence 348, App
C 42	11	37.9	29	US-09-670-075A-8	Sequence 8, Appl
C 43	11	37.9	30	US-08-361-337-50	Sequence 50, Appl
C 44	11	37.9	30	US-09-470-661A-38	Sequence 38, Appl
45	11	37.9	32	US-07-931-473B-331	Sequence 331, App

ALIGNMENTS

RESULT 1  
US-08-316-293-53  
; Sequence 53, Application US/08316293  
; Patent No 5484599  
; GENERAL INFORMATION:  
; APPLICANT: ABBOTT LABORATORIES  
; APPLICANT: Stanley R. Bouma  
; APPLICANT: Thomas G. Laffler  
; APPLICANT: Ronald L. Marshall  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES USEFUL AS  
; TITLE OF INVENTION: TYPE-SPECIFIC PROBES, PCR PRIMERS AND LCR PROBES  
; TITLE OF INVENTION: FOR THE AMPLIFICATION AND DETECTION OF HUMAN  
; TITLE OF INVENTION: PAPILLOMA VIRUS, AND RELATED KITS AND METHODS.  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: One Abbott Park Road  
; CITY: Abbott Park  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/316,293  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/965,665  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas D. Brainard  
; REGISTRATION NUMBER: 32,459  
; REFERENCE/DOCKET NUMBER: 4853.US.P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (708) 937-4884  
; TELEFAX: (708) 937-9556  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)

US-08-316-293-53

Query Match 48.3%; Score 14; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGGTGATATGCT 14  
|||||  
DB 1 GATGGTGATATGCT 14

RESULT 2

US-09-757-207-1

; Sequence 1, Application US/09757207  
; Patent No. 6770752  
; GENERAL INFORMATION:  
; APPLICANT: Hellyer, Tobin J.  
; APPLICANT: You, Qimin  
; APPLICANT: Harris, James M.  
; TITLE OF INVENTION: Sequences and Methods for Detection of HIV-1  
; FILE REFERENCE: Seq/Mtds for Detection of HIV-1  
; CURRENT APPLICATION NUMBER: US/09/757,207  
; CURRENT FILING DATE: 2001-01-09  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-757-207-1

Query Match 44.8%; Score 13; DB 3; Length 41;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGTAGATACAGGA 24  
|||||  
DB 23 GGTAGATACAGGA 35

RESULT 3

US-09-198-452A-3549

; Sequence 3549, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Grifais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 3549  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-3549

Query Match 41.4%; Score 12; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GATACAGGATTT 27  
|||||  
DB 2 GATACAGGATTT 13

RESULT 4

US-08-358-171-13/c

; Sequence 13, Application US/08358171  
; Patent No. 5763578  
; GENERAL INFORMATION:

; APPLICANT: FONG, Henry K.W.  
; TITLE OF INVENTION: ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA  
; TITLE OF INVENTION: ENCODING SAME, AND ANTIBODIES THEREO  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/358,171  
; FILING DATE: 16-DEC-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: FONG=2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: oligonucleotide  
US-08-358-171-13

Query Match 41.4%; Score 12; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TAGATACAGGAT 25  
|||||  
DB 13 TAGATACAGGAT 2

RESULT 5

US-09-090-947-13/c  
; Sequence 13, Application US/09090947  
; Patent No. 6008338  
; GENERAL INFORMATION:  
; APPLICANT: FONG, Henry K.W.  
; TITLE OF INVENTION: ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/090,947  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/358,171

;; FILING DATE: 1998-09-17  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: YUN, Allen C.  
;; REGISTRATION NUMBER: 37,971  
;; REFERENCE/DOCKET NUMBER: FONG=2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-628-5197  
;; TELEFAX: 202-737-3528  
;; TELEX: 248633  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 21 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: oligonucleotide  
US-09-090-947-13

Query Match 41.4%; Score 12; DB 3; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TAGATACAGGAT 25  
DB 13 TAGATACAGGAT 2

RESULT 6  
US-09-396-196G-36348  
; Sequence 36348, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36348  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-36348

Query Match 41.4%; Score 12; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGGTGATGATGGT 14  
DB 11 TGGTGATGATGGT 22

RESULT 7  
US-09-396-196G-73518/c  
; Sequence 73518, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678

;; PRIOR FILING DATE: 1998-09-17  
;; NUMBER OF SEQ ID NOS: 127806  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 73518  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: mus musculus  
US-09-396-196G-73518

Query Match 41.4%; Score 12; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGATATGGTAGA 17  
DB 23 TGATATGGTAGA 12

RESULT 8  
US-09-396-196G-73519/c  
; Sequence 73519, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 73519  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-73519

Query Match 41.4%; Score 12; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGATATGGTAGA 17  
DB 20 TGATATGGTAGA 9

RESULT 9  
US-09-396-196G-81905/c  
; Sequence 81905, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.

;; TITLE OF INVENTION: Methods of Genetic Analysis  
;; FILE REFERENCE: 3101.1  
;; CURRENT APPLICATION NUMBER: US/09/396,196G  
;; CURRENT FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: 60/100,678  
;; PRIOR FILING DATE: 1998-09-17  
;; NUMBER OF SEQ ID NOS: 127806  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 81905  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: mus musculus  
US-09-396-196G-81905

Query Match 41.4%; Score 12; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GTAGATACAGGA 24  
|||||  
DB 21 GTAGATACAGGA 10

RESULT 10  
US-09-396-196G-94653/c  
; Sequence 94653, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 94653  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-94653

Query Match 41.4%; Score 12; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGATATGGTAGA 17  
|||||  
DB 23 TGATATGGTAGA 12

RESULT 11  
US-09-396-196G-94664/c  
; Sequence 94664, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 94664  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-94664

Query Match 41.4%; Score 12; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGATATGGTAGA 17  
|||||  
DB 21 TGATATGGTAGA 10

RESULT 12  
US-09-396-196G-94665/c  
; Sequence 94665, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 94665  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-94665

Query Match 41.4%; Score 12; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGATATGGTAGA 17  
|||||  
DB 19 TGATATGGTAGA 8

RESULT 13  
US-09-513-999C-22225  
; Sequence 22225, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59 US2 REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 22225  
; LENGTH: 98  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-513-999C-22225

Query Match 41.4%; Score 12; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGATATGGTAG 16  
|||||  
DB 20 GTGATATGGTAG 31

RESULT 14  
US-09-021-701-1077/c  
; Sequence 1077, Application US/09021701  
; Patent No. 6251588  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Karen W.  
; APPLICANT: Wolber, Paul K.  
; APPLICANT: Delenstarr, Glenda C.  
; APPLICANT: Webb, Peter G.

APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
TITLE OF INVENTION: probe sequences  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/021,701  
FILING DATE: 10-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-236-2386  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 1077:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-021-701-1077

Query Match 37.9%; Score 11; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TAGATACAGGA 24  
|||||  
DB 20 TAGATACAGGA 10

RESULT 15  
US-09-021-701-1078/c  
Sequence 1078, Application US/09021701  
Patent No. 6251588  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Delenstarr, Glenda C.  
APPLICANT: Webb, Peter G.  
APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
TITLE OF INVENTION: probe sequences  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/021,701  
FILING DATE: 10-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-236-2386  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 1078:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-021-701-1078

Query Match 37.9%; Score 11; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TAGATACAGGA 24  
|||||  
DB 19 TAGATACAGGA 9

Search completed: March 5, 2006, 19:10:48  
Job time : 79 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 19:08:04 ; Search time 78 Seconds  
(without alignments)  
660.888 Million cell updates/sec

Title: US-10-720-424B-8

Perfect score: 29

Sequence: 1 ggcgcagaggtaccatagagccactagg 29

Scoring-table: OLIGO-NUC

Gapop-60.0, Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word-size: 1

Total number of hits satisfying chosen parameters: 1426356

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:\*

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- 2: /cgn2\_6/prodata/1/ina/5 COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/6A COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/H COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/PCTUS COMB.seq:\*
- 7: /cgn2\_6/prodata/1/ina/PP COMB.seq:\*
- 8: /cgn2\_6/prodata/1/ina/RE COMB.seq:\*
- 9: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	41.4	19	3	US-09-696-791-3968
2	12	41.4	19	3	US-09-696-791-3968
3	12	41.4	19	3	US-09-696-791-3970
4	12	41.4	25	3	US-09-396-196G-22482
5	12	41.4	25	3	US-09-396-196G-59285
6	12	41.4	25	3	US-09-396-196G-79525
7	11	37.9	18	2	US-08-190-199A-33
8	11	37.9	19	3	US-09-422-978-4722
9	11	37.9	20	2	US-07-922-723A-6
10	11	37.9	20	2	US-07-799-828C-6
11	11	37.9	20	2	US-08-074-278-6
12	11	37.9	20	2	US-08-480-366-6
13	11	37.9	20	2	US-07-952-277A-6
14	11	37.9	20	3	US-09-283-040-8
15	11	37.9	20	3	US-09-413-304-9
16	11	37.9	20	3	US-09-659-791A-76
17	11	37.9	20	3	US-09-817-856-9
18	11	37.9	20	3	US-09-780-175-144
19	11	37.9	23	3	US-09-167-681-19
20	11	37.9	23	3	US-10-164-230-17
21	11	37.9	25	3	US-09-396-196G-8219
22	11	37.9	25	3	US-09-396-196G-20870
23	11	37.9	25	3	US-09-396-196G-20872
24	11	37.9	25	3	US-09-396-196G-42248

C 25	11	37.9	25	3	US-09-396-196G-84796	Sequence 84796, A
C 26	11	37.9	25	3	US-09-396-196G-84797	Sequence 84797, A
C 27	11	37.9	25	3	US-09-396-196G-84813	Sequence 84813, A
C 28	11	37.9	25	3	US-09-396-196G-84814	Sequence 84814, A
C 29	11	37.9	25	3	US-09-396-196G-87409	Sequence 87409, A
C 30	11	37.9	25	3	US-09-396-196G-87420	Sequence 87420, A
C 31	11	37.9	25	3	US-09-396-196G-87421	Sequence 87421, A
C 32	11	37.9	25	3	US-09-396-196G-87422	Sequence 87422, A
C 33	11	37.9	25	3	US-09-396-196G-95386	Sequence 95386, A
C 34	11	37.9	25	3	US-09-396-196G-118491	Sequence 118491, A
C 35	11	37.9	25	3	US-09-396-196G-118492	Sequence 118492, A
C 36	11	37.9	39	3	US-09-452-638-46	Sequence 46, Appl
C 37	11	37.9	43	3	US-09-641-638-780	Sequence 780, Appl
C 38	11	37.9	44	3	US-10-170-097-780	Sequence 780, Appl
C 39	11	37.9	44	3	US-09-354-409-3	Sequence 3, Appl
C 40	11	37.9	45	2	US-08-853-217-22	Sequence 22, Appl
C 41	11	37.9	46	2	US-08-495-695B-14	Sequence 14, Appl
C 42	11	37.9	46	3	US-09-430-775-14	Sequence 14, Appl
C 43	11	37.9	46	6	PCT-US94-14436-14	Sequence 14, Appl
C 44	11	37.9	47	3	US-09-422-978-2911	Sequence 2911, Appl
C 45	11	37.9	54	2	US-08-311-486C-1123	Sequence 1123, Appl

ALIGNMENTS

RESULT 1  
US-09-696-791-3968  
; Sequence 3968, Application US/09696791  
; Patent No. 6770633  
; GENERAL INFORMATION:  
; APPLICANT: Robbins, Joan M.  
; APPLICANT: Tritz, Richard  
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: SKIN AND EYE DISEASES  
; FILE REFERENCE: 480124.407  
; CURRENT APPLICATION NUMBER: US/09/696,791  
; CURRENT FILING DATE: 2000-10-25  
; NUMBER OF SEQ ID NOS: 4523  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3968  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: PCNA HH ribozyme binding site  
US-09-696-791-3968

Query Match 41.4%; Score 12; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 GTTACCATAGAG 21  
DB 8 GTTACCATAGAG 19  
RESULT 2  
US-09-696-791-3969  
; Sequence 3969, Application US/09696791  
; Patent No. 6770633  
; GENERAL INFORMATION:  
; APPLICANT: Robbins, Joan M.  
; APPLICANT: Tritz, Richard  
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: SKIN AND EYE DISEASES  
; FILE REFERENCE: 480124.407  
; CURRENT APPLICATION NUMBER: US/09/696,791  
; CURRENT FILING DATE: 2000-10-25  
; NUMBER OF SEQ ID NOS: 4523  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3969  
; LENGTH: 19

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-3969

Query Match      41.4%; Score 12; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTACCATAG 21
Db 7 GTTACCATAG 18

RESULT 3
US-09-696-791-3970
; Sequence 3970, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3970
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-3970

Query Match      41.4%; Score 12; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTACCATAG 21
Db 2 GTTACCATAG 13

RESULT 4
US-09-396-196G-22482
; Sequence 22482, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22482
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-22482

Query Match      41.4%; Score 12; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTACCATAG 21
Db 2 GTTACCATAG 13

RESULT 5
US-09-396-196G-59285/c
; Sequence 59285, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59285
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-59285

Query Match      41.4%; Score 12; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ACCATAGAGCCA 24
Db 14 ACCATAGAGCCA 3

RESULT 6
US-09-396-196G-79525/c
; Sequence 79525, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79525
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-79525

Query Match      41.4%; Score 12; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTACCATAG 21
Db 23 GTTACCATAG 12

RESULT 7
US-08-190-199A-33
; Sequence 33, Application US/08190199A
; Patent No. 5830663
```



GENERAL INFORMATION:  
APPLICANT: EMBLETON, Michael J.  
APPLICANT: GORCHOV, Guy  
APPLICANT: JONES, Peter T.  
APPLICANT: WINTER, Gregory P.  
TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/190,199A  
FILING DATE: 13-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/01483  
FILING DATE: 10-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9212419.7  
FILING DATE: 11-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9117352.6  
FILING DATE: 10-AUG-1991  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-190-199A-33

Query Match 37.9%; Score 11; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TACCATAGGC 22  
DB 4 TACCATAGGC 14

RESULT 8  
US-09-422-978-4722  
Sequence 4722, Application US/09422978  
Patent No. 6537751  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
FILE REFERENCE: GENSET.020CP1  
CURRENT APPLICATION NUMBER: US/09/422,978  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 4722  
LENGTH: 19

TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 1..19  
OTHER INFORMATION: upstream amplification primer 99-17343 for SEQ 788,  
US-09-422-978-4722

Query Match 37.9%; Score 11; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTTACCATAG 19  
DB 9 GGTTACCATAG 19

RESULT 9  
US-07-922-723A-6/c  
Sequence 6, Application US/07922723A  
Patent No. 5369004  
GENERAL INFORMATION:  
APPLICANT: Drs. Michael H. Polymeropoulos  
APPLICANT: and Carl R. Merrill  
TITLE OF INVENTION: FIVE HIGHLY INFORMATIVE  
TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lowe, Price, LeBlanc & Becker  
STREET: Suite 300, 99 Canal Center Plaza  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: DOS Text File  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/922,723A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: D.J. Mills  
REGISTRATION NUMBER: 34506  
REFERENCE/DOCKET NUMBER: 717081B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703 684 1111  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-922-723A-6

Query Match 37.9%; Score 11; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CATAGAGCCAC 25  
DB 18 CATAGAGCCAC 8

RESULT 10  
US-07-799-828C-6/c  
Sequence 6, Application US/07799828C  
Patent No. 5378602  
GENERAL INFORMATION:  
APPLICANT: Drs. Carl R. Merrill and

APPLICANT: Mihael H. Polymeropoulos  
TITLE OF INVENTION: TWENTY SEVEN HIGHLY INFORMATIVE  
TITLE OF INVENTION: MICROSATELLITE REPEAT  
TITLE OF INVENTION: POLYMORPHIC DNA MARKERS  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lowe, Price, LeBlanc & Becker  
STREET: Suite 300, 99 Canal Center Plaza  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: DOS Text File  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/799,828C  
FILING DATE: 19911127  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: D.J. Mills  
REGISTRATION NUMBER: 34,506  
REFERENCE/DOCKET NUMBER: 717081A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703 684 1111  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-799-828C-6

Query Match 37.9%; Score 11; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CATAGAGCCAC 25  
DB 18 CATAGAGCCAC 8

RESULT 11  
US-08-074-275-6/c  
Sequence 6, Application US/08074275  
Patent No. 5486610  
GENERAL INFORMATION:  
APPLICANT: Drs. Carl R. Merrill and  
APPLICANT: Mihael H. Polymeropoulos  
TITLE OF INVENTION: THREE HIGHLY INFORMATIVE REPEAT  
TITLE OF INVENTION: POLYMORPHIC DNA MARKERS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lowe, Price, LeBlanc & Becker  
STREET: Suite 300, 99 Canal Center Plaza  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: DOS Text File  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/074,275  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/707,501

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: J.G. Mullins  
REGISTRATION NUMBER: 33073  
REFERENCE/DOCKET NUMBER: 717081  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703 684 1111  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-074-275-6

Query Match 37.9%; Score 11; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CATAGAGCCAC 25  
DB 18 CATAGAGCCAC 8

RESULT 12  
US-08-480-366-6/c  
Sequence 6, Application US/08480366  
Patent No. 5721100  
GENERAL INFORMATION:  
APPLICANT: Drs. Carl R. Merrill and  
APPLICANT: Mihael H. Polymeropoulos  
TITLE OF INVENTION: THREE HIGHLY INFORMATIVE REPEAT  
TITLE OF INVENTION: POLYMORPHIC DNA MARKERS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lowe, Price, LeBlanc & Becker  
STREET: Suite 300, 99 Canal Center Plaza  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: DOS Text File  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,366  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: J.G. Mullins  
REGISTRATION NUMBER: 33073  
REFERENCE/DOCKET NUMBER: 717081  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703 684 1111  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-480-366-6

Query Match 37.9%; Score 11; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CATAGAGCCAC 25  
DB 18 CATAGAGCCAC 8

RESULT 13  
US-07-952-277A-6/c  
; Sequence 6, Application US/07952277A  
; Patent No. 5861504  
; GENERAL INFORMATION:  
; APPLICANT: Drs. Mhael H. Polymeropoulos  
; APPLICANT: and Carl R. Merrill  
; TITLE OF INVENTION: ELEVEN HIGHLY INFORMATIVE  
; TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lowe, Price, LeBlanc & Becker  
; STREET: Suite 300, 99 Canal Center Plaza  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: DOS Text File  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/07/952,277A  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: D.J. Mills  
; REGISTRATION NUMBER: 34506  
; REFERENCE/DOCKET NUMBER: 717081C  
; TELEPHONE: 703 684 1111  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-07-952-277A-6

Query Match 37.9%; Score 11; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CATAGAGCCAC 25  
Db 18 CATAGAGCCAC 8

RESULT 14  
US-09-283-040-8/c  
; Sequence 8, Application US/09283040  
; Patent No. 6162604  
; GENERAL INFORMATION:  
; APPLICANT: Jacob, C.  
; TITLE OF INVENTION: METHODS FOR DETERMINING GENETIC  
; TITLE OF INVENTION: PREDISPOSITION TO SYSTEMIC LUPUS ERYTHEMATOSUS AND OTHER  
; TITLE OF INVENTION: AUTOIMMUNE DISEASES BY GENOTYPING IL-10, BCL-2, FAS-L, AND  
; TITLE OF INVENTION: OTHER APOPTOTIC GENES.  
; FILE REFERENCE: IMSCI.010A  
; CURRENT APPLICATION NUMBER: US/09/283,040  
; CURRENT FILING DATE: 1999-04-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer to CTLA-4 microsatellite.

; PUBLICATION INFORMATION:  
; AUTHORS: Polymeropoulos, et al.  
; JOURNAL: Nucleic Acids Research  
; VOLUME: 19  
; ISSUE: 1991  
; PAGES: 4018  
US-09-283-040-8

Query Match 37.9%; Score 11; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CATAGAGCCAC 25  
Db 18 CATAGAGCCAC 8

RESULT 15  
US-09-413-304-9/c  
; Sequence 9, Application US/09413304  
; Patent No. 6207387  
; GENERAL INFORMATION:  
; APPLICANT: Louis J. Elias II  
; APPLICANT: K. Muralidharan  
; TITLE OF INVENTION: MOLECULAR DIAGNOSTICS FOR GALACTOSEMIA  
; FILE REFERENCE: 05010.0079  
; CURRENT APPLICATION NUMBER: US/09/413,304  
; CURRENT FILING DATE: 1999-10-06  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. 6207387e =  
US-09-413-304-9

Query Match 37.9%; Score 11; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TAGAGCCACTA 27  
Db 13 TAGAGCCACTA 3

Search completed: March 5, 2006, 19:10:48  
Job time : 78 secs

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GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:20:14 ; Search time 2987.5 Seconds  
(without alignments)  
454.167 Million cell updates/sec

Title: US-10-720-424B-8

Perfect score: 29

Sequence: 1 gcgtcagaggtaccatagaccactagg 29

Scoring-table: OLIGO NUC

Gapop 60.0, Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word-size: 11

Total number of hits satisfying chosen parameters: 777740

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_est3:\*
- 4: gb\_hic:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_est7:\*
- 9: gb\_gss1:\*
- 10: gb\_gss2:\*
- 11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	13	44.8	78	9 AZ422866	AZ422866 IM0201C08
C 3	13	44.8	91	11 CK359087	CK359087 Arabidops
C 4	13	44.8	96	9 B07639	B07639 CDC1e4 Cr1
C 5	12	41.4	44	9 AZ801332	AZ801332 2M0059E17
C 6	12	41.4	69	10 BX288836	BX288836 Arabidops
C 7	12	41.4	71	10 AL768653	AL768653 Arabidops
C 8	12	41.4	75	7 CK589249	CK589249 IST WIS_4
C 9	12	41.4	76	6 CF800008	CF800008 RPL3i-1f
C 10	12	41.4	76	10 C2259321	C2259321 CC0712 Sa
C 11	12	41.4	80	9 BH221305	BH221305 1006100E1
C 12	12	41.4	80	10 AL947277	AL947277 Arabidops
C 13	12	41.4	81	5 BU101523	BU101523 PRODIGID
C 14	12	41.4	83	9 AZ830956	AZ830956 2M0110P22
C 15	12	41.4	83	10 AU595832	AU595832 Arabidops
C 16	12	41.4	89	9 BH860887	BH860887 Gm STR000
C 17	12	41.4	90	1 AA832122	AA832122 oc97h09.s
C 18	12	41.4	91	1 AV563280	AV563280 AV563280
C 19	12	41.4	93	10 CG529767	CG529767 OST110652
C 20	12	41.4	95	10 BX896965	BX896965 Arabidops
C 21	12	41.4	96	5 BU873739	BU873739 Q059D03 P
C 22	12	41.4	97	10 AL942821	AL942821 Arabidops

C 23 12 41.4 98 5 BU831039 BU831039 T016D07 P  
C 24 12 41.4 99 6 CD954464 CD954464 SBO\_322 G  
C 25 12 41.4 99 8 W08501 W08501 mb47d12.r1  
C 26 12 41.4 100 1 A1040719 A1040719 ox26b10.s  
C 27 12 41.4 100 7 CK895114 CK895114 SGP154364  
C 28 12 41.4 100 7 CK896099 CK896099 SGP158635  
C 29 11 37.9 49 1 AA234629 AA234629 xz75b05.r  
C 30 11 37.9 50 10 CW020438 CW020438 GC0700 TI  
C 31 11 37.9 50 11 CR217452 CR217452 Reverse s  
C 32 11 37.9 51 9 BZ382023 BZ382023 SALK\_1177  
C 33 11 37.9 51 10 CW083054 CW083054 104\_425.1  
C 34 11 37.9 53 6 CF660841 CF660841 CCLM09a32  
C 35 11 37.9 56 9 AZ807027 AZ807027 2M0069A03  
C 36 11 37.9 60 1 AU654040 AU654040 AJ654040  
C 37 11 37.9 62 10 BX530887 BX530887 Arabidops  
C 38 11 37.9 63 7 CK814651 CK814651 Rasg8C531  
C 39 11 37.9 63 9 AZ609630 AZ609630 IM0434E04  
C 40 11 37.9 66 10 BX205284 BX205284 Danio rer  
C 41 11 37.9 67 5 BX553131 BX553131 Arabidops  
C 42 11 37.9 67 10 AL751479 AL751479 Arabidops  
C 43 11 37.9 67 10 CG532847 CG532847 OST117308  
C 44 11 37.9 68 10 BX572204 BX572204 Arabidops  
C 45 11 37.9 69 10 BX536465 BX536465 Arabidops

## ALIGNMENTS

RESULT 1  
BX891062/c  
LOCUS BX891062 75 bp DNA linear GSS 05-APR-2004  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-445F03-023515,  
genomic survey sequence.  
ACCESSION BX891062  
VERSION BX891062.1 GI:39923557  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (chale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.  
REFERENCE 1  
Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P., and Weisshaar,B.  
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for  
the identification of T-DNA insertion mutants in Arabidopsis  
thaliana  
Bioinformatics 19 (11), 1441-1442 (2003)  
JOURNAL PUBMED 12874060  
REFERENCE 2  
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and  
Weisshaar,B.  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for  
flanking sequence tag-based reverse genetics  
Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
14756321  
REFERENCE 3  
Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and  
Weisshaar,B.  
High-throughput generation of sequence indexes from T-DNA  
mutagenized Arabidopsis thaliana lines  
Biotechniques 35 (6), 1164-1168 (2003)  
14682050  
4 (bases 1 to 75)  
Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B.  
Direct Submission  
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer  
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA.  
It indicates an insertion close to or within gene At5g44170.  
Details on the protocols used for generation of the sequence are  
described in References 1-3. The sequences are generated at the MPI  
for Plant Breeding Research in the context of the GABI-Kat project.  
GABI-Kat is part of the German Plant Genomics program designated

'GABI'. Information on line availability can be found at:

<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

#### FEATURES

source  
1. .75  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-445F03-023515"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

#### ORIGIN

Query Match 44.8%; Score 13; DB 10; Length 75;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGGTTACCATAG 19  
|||||  
Db 64 GAGGTTACCATAG 52

#### RESULT 2

AZ422866  
LOCUS 78 bp DNA linear GSS 03-OCT-2000  
DEFINITION IM0201C08R Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCGIM0201C08 R, genomic survey sequence.

ACCESSION AZ422866  
VERSION AZ422866.1 GI:10546795

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 78)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0201 row: C column: 08

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 78.

Location/Qualifiers

#### FEATURES

source  
1. .78

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0201C08"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### ORIGIN

Query Match 44.8%; Score 13; DB 9; Length 78;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AGGTTACCATAGA 20  
|||||  
Db 42 AGGTTACCATAGA 54

#### RESULT 3

CR359087/c

LOCUS CR359087.1

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-733D10-025420, genomic survey sequence.

ACCESSION CR359087

VERSION CR359087.1 GI:45542009

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE 1

AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.

TITLE GABI-kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

PUBMED 12874060

REFERENCE 2

AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)

PUBMED 14756321

REFERENCE 3

AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weisshaar,B.

TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

PUBMED 14682050

REFERENCE 4

AUTHORS Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B.

TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At2g36870. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

## FEATURES

source

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1. .91
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_lib="GK-733D10-025420"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pGAB1 (GenBank accession number: AY529716). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

```

## ORIGIN

```

Query Match          44.8%; Score 13; DB 11; Length 91;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 12 TACCATAGAGCCCA 24

Db 54 TACCATAGAGCCCA 42

## RESULT 4

LOCUS

```

DEFINITION
B07639 Crie du chat, exon trapped products Homo sapiens genomic
clone CDC1e4, genomic survey sequence.

```

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

```

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 96)
Church,D.M., Yang,J., Shiang,R., Wasmuth and J.J.
A High Resolution Physical and Transcription map for the Crie du
chat region of human chromosome 5p
Unpublished (1997)
Contact: Rita Shiang
Shiang lab
University of California- Irvine
240D Med. Sci. I, UCI-COM, Irvine, CA 92697-1700, USA
Tel: (714)824-6792
Fax: (714)824-3403
Email: rshiang@chom5.hs.uci.edu
Insert Length: 96 Std Error: 0.00
Class: exon-trapped.

```

## FEATURES

source

```

1. .96
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="CDC1e4"
/notes="Exon trapped products from the CDC critical region associated with mental retardation and facial dysmorphism."

```

## ORIGIN

```

Query Match          44.8%; Score 13; DB 9; Length 96;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 7 GAGGTTACCATAG 19

Db

72 GAGGTTACCATAG 84

RESULT 5

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 44)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0059 row: E column: 17

Seq primer: CACACGAGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 44.

Location/Qualifiers

1. 44

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUC2M0059E17"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match

Best Local Similarity

Matches 12; Conservative

41.4%; Score 12; DB 9; Length 44;

100.0%; Pred. No. 1.9e+04;

Mismatches 0; Indels 0; Gaps 0;

QY 13 ACCATAGGCCA 24  
 |||||  
 Db 24 ACCATAGGCCA 13

RESULT 6  
 BX288836/c 69 bp DNA linear GSS 02-APR-2004  
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-420D05-018101,  
 DEFINITION genomic survey sequence.  
 ACCESSION BX288836  
 VERSION BX288836.1 GI:28887832  
 KEYWORDS GSS  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1  
 REFERENCE Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., Dekker, K.A. and  
 AUTHORS GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for  
 TITLE the identification of T-DNA insertion mutants in Arabidopsis  
 thaliana  
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)  
 PUBMED 12874060  
 REFERENCE 2  
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and  
 Weisshaar, B.  
 TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for  
 JOURNAL flanking sequence tag-based reverse genetics  
 PUBMED Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 REFERENCE 3  
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and  
 Weisshaar, B.  
 TITLE High-throughput generation of sequence indexes from T-DNA  
 JOURNAL mutagenized Arabidopsis thaliana lines  
 PUBMED Biotechniques 35 (6), 1164-1168 (2003)  
 REFERENCE 4 (bases 1 to 69)  
 AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer  
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 COMMENT This sequence has been recovered from the left border of the T-DNA.  
 It indicates an insertion close to or within gene At1g48700.  
 Details on the protocols used for generation of the sequence are  
 described in References 1-3. The sequences are generated at the MPI  
 for Plant Breeding Research in the context of the GABI-Kat project.  
 GABI-Kat is part of the German Plant Genomics program designated  
 'GABI'. Information on line availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES  
 source  
 1..69  
 Location/Qualifiers  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="GK-420D05-018101"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Col-0"  
 /note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161 (GenBank accession number: AJ537514). The  
 lines contain one or more T-DNA insertions. The DNA  
 fragment(s) resulting from the PCR were directly sequenced  
 to determine the genomic sequence flanking the insertion.  
 T-DNA derived sequences were removed."

ORIGIN  
 Query Match 41.4%; Score 12; DB 10; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCATAGGCCAC 25  
 |||||  
 Db 64 CCATAGGCCAC 53

RESULT 7  
 AL768653/c 71 bp DNA linear GSS 01-APR-2004  
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-076E01-011920,  
 DEFINITION genomic survey sequence.  
 ACCESSION AL768653  
 VERSION AL768653.1 GI:21521772  
 KEYWORDS GSS  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1  
 REFERENCE Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.  
 AUTHORS GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for  
 TITLE the identification of T-DNA insertion mutants in Arabidopsis  
 thaliana  
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)  
 PUBMED 12874060  
 REFERENCE 2  
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and  
 Weisshaar, B.  
 TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for  
 JOURNAL flanking sequence tag-based reverse genetics  
 PUBMED Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 REFERENCE 3  
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and  
 Weisshaar, B.  
 TITLE High-throughput generation of sequence indexes from T-DNA  
 JOURNAL mutagenized Arabidopsis thaliana lines  
 PUBMED Biotechniques 35 (6), 1164-1168 (2003)  
 REFERENCE 4 (bases 1 to 71)  
 AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer  
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 COMMENT This sequence has been recovered from the left border of the T-DNA.  
 It indicates an insertion within the locus defined by BAC clone  
 MRC8. Details on the protocols used for generation of the sequence  
 are described in References 1-3. The sequences are generated at the  
 MPI for Plant Breeding Research in the context of the GABI-Kat  
 project. GABI-Kat is part of the German Plant Genomics program  
 designated 'GABI'. Information on line availability can be found  
 at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES  
 source  
 1..71  
 Location/Qualifiers  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="GK-076E01-011920"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Col-0"  
 /note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161 (GenBank accession number: AJ537514). The  
 lines contain one or more T-DNA insertions. The DNA  
 fragment(s) resulting from the PCR were directly sequenced  
 to determine the genomic sequence flanking the insertion.  
 T-DNA derived sequences were removed."

ORIGIN  
 Query Match 41.4%; Score 12; DB 10; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

QY 14 CCATAGGCCAC 25
Db 55 CCATAGGCCAC 44
|||||

RESULT 8
CK589249
LOCUS
DEFINITION
CK589249
ACCESSION
CK589249.1 GI:40973178
VERSION
KEYWORDS
SOURCE
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Pelodierinae; Caenorhabditis.
1 (bases 1 to 75)
REFERENCE
AUTHORS
Li, S., Armstrong, C.M., Bertin, N., Ge, H., Milstein, S., Boxem, M.,
Vidalain, P.O., Han, J.D., Chesneau, A., Hao, T., Goldberg, D.S., Li, N.,
Martinez, M., Rual, J.F., Lamesch, P., Xu, L., Tewari, M., Wong, S.L.,
Zhang, L.V., Berri, G.F., Jacotot, L., Vaglio, P., Reboul, J.,
Hirozane-Kishikawa, T., Li, Q., Gabel, H.W., Elewa, A., Baumgartner, B.,
Rose, D.J., Yu, H., Bosak, S., Sequerra, R., Fraser, A., Mango, S.E.,
Saxton, W.M., Strome, S., Van Den Heuvel, S., Piano, P.,
Vandenhaute, J., Sardet, C., Gerstein, M., Doucette-Stamm, L.,
Gonsky, K.C., Harper, J.W., Cusick, M.E., Roth, F.P., Hill, D.E. and
Vidal, M.
TITLE
A Map of the Interactome Network of the Metazoan C. elegans
JOURNAL
Science (2004) In press
COMMENT
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
For the purpose of protein interaction mapping, we generated a C.
elegans a normalized library of ORF fused to the AD-encoding
sequence of the yeast transcription factor GAL4. Those ORFs derive
from the PCR amplification between the predicted (WS9) initiation
and termination codons, using the cDNA library AD-wrmcDNA as
template. This Interacting Sequence Tag IST-WS9_41889 (F09F7.5)
interacts as a prey with the bait W09H1.6
PCR Primers
FORWARD: CGCGTTGGAATCACTACAGGG
BACKWARD: GGAGCTTGACCAACCTCTGGCG
Insert Length: 75 Std Error: 74.00
Plate: 547 row: 08 column: H
Seq primer: CGCGTTGGAATCACTACAGGG
High quality sequence stop: 74
POLYA=No.
FEATURES
Location/Qualifiers
1..75
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="male, hermaphrodite"
/dev_stage="embryos, L1, L2, L3, L4, adult, dauer"
/clone_lib="AD-ORFeome1.0 library"
/note="Vector: pDestPC86/Cyh; For the purpose of protein
interaction mapping, predicted protein-encoding ORFs were
amplified by PCR precisely between the predicted (WS9)
version of WormPep) initiation and termination codons,
using a cDNA library (AD-wrmcDNA library - Walhout et al,
Methods Enzymol. 2000;328:575-92) as template. The
resulting 11,984 Gateway cloned ORFs along with the
attempted ones were transferred into a two-hybrid
Destination vector downstream of the vector sequence
encoding the activation domain (AD) of the yeast GAL4
transcription factor. Those constructs were pooled
together to constitute a 'normalized' AD-ORFeome1.1
library. Reference - Reboul J, Vaglio P et al C. elegans
ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression. Nat Genet. 2003 May;34(1):35-41. PMID:
12679813)"
ORIGIN
Query Match 41.4%; Score 12; DB 7; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GTCAGAGGTTAC 14
Db 40 GTCAGAGGTTAC 51
|||||

RESULT 9
CF800008/c
LOCUS
DEFINITION
Rpl31-II-B7 Rpl31 Rhopalosiphum padi cDNA clone Rpl31II7B 5', mRNA
sequence.
ACCESSION
CF800008
VERSION
CF800008.1 GI:37804578
KEYWORDS
EST.
SOURCE
Rhopalosiphum padi (bird cherry-oat aphid)
Rhopalosiphum padi
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Aphidini; Rhopalosiphum.
1 (bases 1 to 76)
REFERENCE
AUTHORS
Tagu, C., Prunier-Leterme, N., Legai, F., Gauthier, J.P., Duclert, A.,
Sabater-Munoz, B., Bonhomme, J. and Simon, J.C.
TITLE
Annotated expressed sequence tags for studies of the regulation of
reproductive modes in aphids
JOURNAL
Insect. Biochem. Mol. Biol. 34 (8), 809-822 (2004)
COMMENT
15362285
Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
PCR Primers
FORWARD: CGCGATTAACCTCGTATAGCA
Plate: II row: B column: 7.
FEATURES
Location/Qualifiers
1..76
/organism="Rhopalosiphum padi"
/mol_type="mRNA"
/strain="h3"
/db_xref="taxon:40932"
/clone="Rpl31II7B"
/tissue_type="whole insect"
/dev_stage="third instar nymph (L3)"
/lab_host="TOF10"
/clone_lib="Rpl31"
/note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;
aphids inoculated on one-week old wheat germinations in
test tube under non sterile conditions. experimental
condition: short photoperiod (10-hr light/14-hr dark at
12oC during 12 days)"
ORIGIN
Query Match 41.4%; Score 12; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 ACCATAGAGCCA 24
Db 72 ACCATAGAGCCA 61
|||||

RESULT 10
C2259321/c

```



described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

#### FEATURES

source  
1..80  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-303A11-015563"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

#### ORIGIN

Query Match 41.4%; Score 12; DB 10; Length 80;  
Best Local Similarity 100.0%; Pred. No. 1.9e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTACCATGAG 21  
|||||  
DB 42 GTTACCATGAG 31

#### RESULT 13

BUI01523/c  
LOCUS  
DEFINITION  
PRODIGID25R1 Compugen\_targeted\_mRNA\_sequencing Homo sapiens cDNA,  
mRNA sequence.

ACCESSION  
BUI01523

VERSION  
BUI01523.1 GI:45736923

KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
1 (bases 1 to 81)

Xie H., Diber A., Pollack S., Nemzer S., Safer H., Meloon B.,  
Olson A., Hwang J.-J., Endress G.A., Savitsky K. and Gill-More R.  
Bridging expressed sequence alignments through targeted cDNA  
sequencing

JOURNAL  
Genomics 83 (4), 572-576 (2004)

PUBMED  
15028280

COMMENT  
Contact: Xie H

Compugen  
7 Center Drive, Suite 9, Jamesburg, NJ 08831, USA

Tel: 609-655-5105 X 26

Fax: 609-655-5114

Email: han@compugen.com

Location/Qualifiers

#### FEATURES

source  
1..81  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

/clone\_lib="Compugen targeted mRNA sequencing"  
/notes="These sequences resulted from single pass  
sequencing of PCR products from Compugen targeted mRNA  
sequencing project. PCR primers and nested primers were  
designed to join two neighboring expressed sequence  
contigs based on Compugen LEADS expressed sequence  
and assembly platform. Reverse transcriptase PCR and  
nested PCR reactions were performed by Protodyne Inc.  
(Windor, CT 06095, USA) on normal human heart, brain,  
lung, liver, placenta, and testis poly mRNA preparations  
from Origen (Rockville, MD 20850, USA) with reagents from

#### ORIGIN

Query Match 41.4%; Score 12; DB 5; Length 81;  
Best Local Similarity 100.0%; Pred. No. 1.9e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 TACCATAGAGCC 23  
|||||  
DB 39 TACCATAGAGCC 28

#### RESULT 14

AZ830956/c  
LOCUS  
DEFINITION  
2M0110P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0110P22 F, genomic survey sequence.

ACCESSION  
AZ830956

VERSION  
AZ830956.1 GI:13000864

KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

#### REFERENCE

AUTHORS  
1 (bases 1 to 83)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

#### TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

#### JOURNAL

Unpublished (2000)

#### COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0110 row: P column: 22

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 83.

#### FEATURES

Location/Qualifiers

1..83

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0110P22"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to

#### FEATURES

source

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Search completed: March 6, 2006, 00:16:52  
Job time : 2990.5 secs

## ORIGIN

Query Match 41.4%; Score 12; DB 9; Length 83;  
Best Local Similarity 100.0%; Pred. No. 1.9e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 AGGTTACCATAG 19  
|||||  
Db 81 AGGTTACCATAG 70

## RESULT 15

AJ595832  
LOCUS  
DEFINITION  
424E08, genomic survey sequence.  
ACCESSION  
AJ595832  
VERSION  
AJ595832.1 GI:37945460  
KEYWORDS  
GSS; left border; T-DNA flanking sequence.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE

1  
Aubourg, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,  
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,  
Lepiniec, L., Caboche, M. and Leclercq, A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

## TITLE

JOURNAL  
PUBMED  
REFERENCE  
1246565  
2 (bases 1 to 83)  
Balzergue, S.

## AUTHORS

Direct Submission  
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
<http://dbgap.versailles.inra.fr/publiclines/>. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (<http://www.genoplante.com> and  
<http://genoplante-info.inbio.gen.fr>).

## FEATURES

source  
1..83  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="424E08"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Wassilewskija"  
misc\_feature 1..83  
/notes="T-DNA flanking sequence  
left border"

## ORIGIN

Query Match 41.4%; Score 12; DB 10; Length 83;  
Best Local Similarity 100.0%; Pred. No. 1.9e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY 13 ACCATAGAGCCA 24

|||||  
Db 64 ACCATAGAGCCA 75